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OW protein - protein search, using sw model

Run on: November 10, 2004, 18:00:33 / Search time 156 Seconds

(without alignments)
78.185 Million cell updates/sec

Title: US-10-685-435-15

Percent score: 185
Sequence: 1 STYGHITGHRMADMMNMSPTALVVSQILRI 34

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_23804:*

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185	100.0	34	2	AAV39498
2	185	100.0	34	2	AAV14171
3	185	100.0	34	3	AAV69660
4	185	100.0	192	6	AAV55557
5	185	100.0	192	6	AAV32870
6	185	100.0	200	5	AAO18668
7	185	100.0	200	7	ADD55534
8	185	100.0	200	7	ADP71116
9	185	100.0	210	5	AAO18669
10	185	100.0	210	7	ADD55536
11	185	100.0	210	8	ADP71118
12	185	100.0	212	5	AAO18660
13	185	100.0	212	8	ADD55512
14	185	100.0	212	8	ADP71094
15	185	100.0	239	5	AAO18666
16	185	100.0	239	7	ADD55530
17	185	100.0	239	8	ADP71112
18	185	100.0	263	5	AAO18661
19	185	100.0	263	7	ADD55514
20	185	100.0	263	8	ADP71096
21	185	100.0	692	5	AAO18678
22	185	100.0	692	7	ADD55556
23	185	100.0	692	8	ADP71138
24	185	100.0	809	5	AAO18679
25	185	100.0	809	7	ADD55558

26	185	100.0	809	8	ADP71140	Adp71140 HCV E1 pr
27	184	99.5	192	2	AAV69647	AAV69647 Hepatitis
28	184	99.5	192	2	AAV69652	AAV69652 Hepatitis
29	184	99.5	192	2	AAV69656	AAV69656 Hepatitis
30	184	99.5	192	2	AAV69642	AAV69642 Hepatitis
31	184	99.5	192	2	AAV69653	AAV69653 Hepatitis
32	184	99.5	192	2	AAV69657	AAV69657 Hepatitis
33	184	99.5	192	2	AAV69658	AAV69658 Hepatitis
34	184	99.5	192	2	AAV69659	AAV69659 Hepatitis
35	182	98.4	106	3	AAV18532	AAV18532 Protein e
36	182	98.4	106	8	ADN35960	ADN35960 HCV CDNA
37	182	98.4	192	2	AAV69638	AAV69638 Hepatitis
38	182	98.4	192	2	AAV69640	AAV69640 Hepatitis
39	182	98.4	192	2	AAV69634	AAV69634 Hepatitis
40	182	98.4	192	2	AAV69637	AAV69637 Hepatitis
41	182	98.4	192	2	AAV69508	AAV69508 Hepatitis
42	182	98.4	192	2	AAV69511	AAV69511 Hepatitis
43	182	98.4	192	2	AAV69505	AAV69505 Hepatitis
44	182	98.4	192	2	AAV69509	AAV69509 Hepatitis
45	182	98.4	193	2	AAV33984	AAV33984 Tn E1 pro

ALIGNMENTS

RESULT 1
AAV39498
ID AAV39498 standard; peptide; 34 AA.

AC AAV39498;

DT 27-AUG-2003 (revised)
DT 22-NOV-1999 (first entry)

DE HCV E1 protein residues 307-340.

KW HCV; E1 protein; E2 protein; epitope; hepatitis c virus; antibody;
KW detection; HCV protein antigen.

XX Hepatitis C virus.

PD 06-OCT-1999.

PF 27-MAR-1998; 98EP-00870060.

PR 27-MAR-1998; 98EP-00870060..

PA (INNO-) INNOGENETICS NV.

XX WPI; 1999-542955/46.

XX New anti-Hepatitis C virus (HCV) antibodies useful for in situ detection

PT of HCV.

PS Example 4; Page 9; 32pp; English.

XX This sequence represents residues 307-340 of the hepatitis c virus (HCV)
CC E1 protein. The invention relates to an antibody (Ab) or its derivative
CC that specifically binds to the C-terminal region of the HCV E1 protein
CC (amino acids (aa) 227-383) or the N-terminal region of the HCV E2 protein
CC (aa 384-450). The Ab allows the in situ detection of HCV protein
CC antigens. The Ab is used to detect the HCV E1 or E2 proteins in human
CC peripheral blood cells or liver tissue. It may also be used to detect HCV
CC in other tissue and fluid samples such as serum, plasma, saliva, mucus
CC and sections or biopsies such as from skin. (Updated on 27-AUG-2003 to
CC correct OS field.)

XX Sequence 34 AA;

Query March 100.0%; Score 185; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 9e-21;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMMSPTTALVVSQLLRI 34
 DB 1 SIYPGHITGHRAMDMNMMSPTTALVVSQLLRI 34

RESULT 2

AA14171
 ID AAY14171 standard; peptide; 34 AA.

AC AAY14171;

DT 27-AUG-2003 (revised)

DT 27-JUL-1999 (first entry)

DE HCV envelope region peptide C4V6.

KW HCV, envelope peptide; HCV-related virus; diagnosis; infection; vaccine.

OS Hepatitis C virus.

PN WO9924466-A2.

PD 20-MAY-1999.

PF 06-NOV-1998; 98WO-EP007105.

PR 06-NOV-1997; 97EP-00870179.

PA (INNO-) INNOGENETICS NV.

PI Maertens G, Depla E;

DR WPI; 1999-327360/27.

PT Peptides from the envelope protein of hepatitis C-related viruses.

PS Claim 2; Page 28; 50pp; English.

CC This sequence represents a HCV envelope region peptide of the invention.
 CC The peptides: (i) contain more than 20 contiguous amino acids (aa)
 CC derived from the envelope region of a hepatitis C virus (HCV)-related
 CC virus (A); and (ii) bind and recognize anti-(A) antibodies (Ab), also
 CC their functionally equivalent fragments or variants. The peptides are
 CC used: (i) to detect Ab in usual immunoassays, for diagnosing exposure to,
 CC or infection by, (A); (ii) for identifying modulators (ii) of peptide-Ab
 CC interaction. Also the peptides, (ii) and vectors that express nucleic
 CC acids encoding them, are useful as vaccines to protect humans against (A)
 CC or their mutant strains. The peptides recognise most anti-HCV antibodies
 CC directed against E1 and E2 proteins in the serum; contrast smaller known
 CC peptides or similar peptides expressed in prokaryotes. (Updated on 27-AUG
 CC -2003 to correct OS field.)

SO Sequence 34 AA;

Query Match 100.0%; Score 185; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 9e-21;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMMSPTTALVVSQLLRI 34
 DB 1 SIYPGHITGHRAMDMNMMSPTTALVVSQLLRI 34

RESULT 3

AA69660
 ID AAY69660 standard; protein; 34 AA.

AC AAY69660;

DT 08-MAY-2000 (first entry)

DE HCV E1 peptide, C4V6, used to map B-cell epitopes.
 KW Envelope protein; oligomeric particle; HCV infection; immunogenic;
 KW cellular immunity; humoral immunity; E1 protein; B-cell epitope mapping;
 KW antigen; antibody; vaccine; treatment; prophylaxis; detection.

OS Hepatitis C virus.

PN WO9967285-A1.

PD 29-DEC-1999.

PF 23-JUN-1999; 99WO-EP04342.

PR 24-JUN-1998; 98EP-00870142.

PR 22-FEB-1999; 99EP-00870033.

PA (INNO-) INNOGENETICS NV.

PI Depla E, Maertens G, Bosman A, Van Wijngaerde F;

DR WPI; 2000-147201/13.

PT Novel HCV envelope protein particles used for vaccination against HCV

infection.

PS Example 5; Page 53; 105pp; English.

CC The invention relates to a novel oligomeric particle comprising hepatitis
 CC C virus (HCV) envelope proteins, with a diameter of 1-100 nm. The
 CC invention also encompasses a purified HCV envelope protein (preferably E1
 CC or E1s), specific antibodies generated against the oligomeric particles,
 CC or a single HCV envelope protein, and methods for detection of HCV
 CC antigens and antibodies. The HCV envelope oligomeric particles are highly
 CC immunogenic when presented to chronic HCV carriers, stimulating both
 CC cellular and humoral responses, and may additionally comprise a T-cell
 CC stimulating antigen such as core protein, E1, E2, NS2, NS3, NS4A, NS4B,
 CC NS5A or NS5B. The oligomeric particle of the invention may be used in
 CC vaccine compositions against HCV and for inducing immunity against HCV in
 CC chronic HCV carriers, especially prior to, simultaneously with, or after
 CC any other therapy. They may be used for inducing immunity against HCV in
 CC HCV-infected individuals prior to or after liver transplantation or after
 CC presumed infection and also for prophylactically inducing immunity
 CC against HCV. Antibodies raised against the oligomeric particles are used
 CC to detect HCV antigens, and to treat or prevent HCV infection. The
 CC oligomeric particles are used to detect HCV antibodies in a sample, and
 CC to detect HCV related T cell responses. Prior art methods for HCV
 CC vaccination have been unsuccessful. Prophylactic vaccination has also
 CC only been shown to be effective against a homologous strain of HCV. The
 CC present invention provides methods for successful vaccination against
 CC HCV. Sequences AAY69655-Y69660 represent HCV E1-derived peptides used to
 CC map B-cell epitopes in an exemplification of the present invention

SO Sequence 34 AA;

Query Match 100.0%; Score 185; DB 3; Length 34;

Best Local Similarity 100.0%; Pred. No. 9e-21;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMMSPTTALVVSQLLRI 34
 DB 1 SIYPGHITGHRAMDMNMMSPTTALVVSQLLRI 34

RESULT 4

ABP5557
 ID ABP5557 standard; protein; 192 AA.

AC ABP5557;

DT 19-FEB-2003 (first entry)

DE Hepatitis C virus protein SEQ ID NO:87.

XX Hepatitis C virus; HCV; envelope protein; hepatotropic; virucide;
 KM antiinflammatory; gene therapy; vaccine.
 XX Hepatitis C virus.
 OS
 XX WO200285932-A2.
 FN
 XX 31-OCT-2002.
 PD
 XX 24-APR-2002; 2002WO-BE000062.
 PF
 XX 24-APR-2001; 2001EP-00870088.
 PR 17-JUL-2001; 2001US-0305604P.
 XX
 XX (INNO-) INNOGENETICS NV.
 PA
 XX Sablon E, Van Broekhoven A, Bosman A, Depia E, Deschamps G;
 PI
 XX WPI; 2003-093095/08.
 DR
 XX New recombinant nucleic acids for expressing Hepatitis C virus (HCV)
 PT envelope proteins in eukaryotic cells, comprising a sequence encoding a
 PT protein having an avian lysozyme leader peptide joined to the HCV
 PT envelope protein.
 XX
 XX Claim 5; Page 306-307; 319pp; English.
 PS
 XX The present invention describes a recombinant nucleic acid (I) comprising
 CC a nucleotide sequence encoding a protein having an avian lysozyme leader
 CC peptide, or its functional equivalent, joined to a Hepatitis C virus
 CC (HCV) envelope protein or its part. Also described: (1) a vector
 CC comprising the recombinant nucleic acid; (2) a host cell comprising the
 CC recombinant nucleic acid or the vector; and (3) a method for producing
 CC HCV envelope protein or its part in a host cell, comprising transforming
 CC the host cell with the recombinant nucleic acid or with the vector, where
 CC the host cell is capable of expressing the protein cited above. (1) has
 CC hepatotropic, virocidic and antiinflammatory activities, and can be used
 CC in gene therapy and vaccines. The recombinant nucleic acid is useful for
 CC efficient expression of Hepatitis C virus envelope proteins in eukaryotic
 CC cells, such as yeast cells. The HCV envelope proteins may be used as a
 CC vaccine, or for incorporation into an immunoassay for the detection of
 CC anti-HCV antibodies; and/or genotyping of HCV, for prognosing or
 CC monitoring of HCV disease, or as a therapeutic agent. The method is used
 CC for producing HCV envelope protein or its part in a host cell. ABQ84197
 CC to ABQ84253 and ABP55528 to ABP55568 represent sequences used in the
 CC exemplification of the present invention
 CC
 XX Sequence 192 AA;
 SQ
 Query Match 100.0%; Score 185; DB 6; Length 192;
 Best Local Similarity 100.0%; Pred. No. 6.9e-20;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
 Db 116 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 149
 RESULT 5
 AAE32870
 ID AAE32870 standard; protein; 192 AA.
 XX
 AC AAE32870;
 XX
 XX 24-MAR-2003 (first entry)
 DT
 XX
 XX Hepatitis C virus protein #5.
 DE
 XX Hepatitis C virus; HCV; envelope protein; virucide; immunostimulant;
 KM immune response; T-cell; therapy; infection; pharmaceutical; vaccine.
 XX Hepatitis C virus.
 OS

XX
 PN WO200286101-A2.
 XX
 PD 31-OCT-2002.
 XX
 XX 24-APR-2002; 2002WO-BE000064.
 PF
 XX 24-APR-2001; 2001EP-00870088.
 PR 17-JUL-2001; 2001US-0305604P.
 XX
 XX (INNO-) INNOGENETICS NV.
 PA
 XX Depia E, Bosman A, Deschamps G, Sablon E, Suckow M, Samson I;
 PI Verheyden G;
 XX WPI; 2003-103409/09.
 DR
 XX New Hepatitis C virus (HCV) envelope protein with N-glycosylation
 PT site(s), useful as a vaccine for inducing a HCV-specific immune response
 PT or HCV-specific antibodies, particularly for preventing or treating HCV
 PT infection.
 XX
 XX Claim 10; Page 333-340; 355pp; English.
 PS
 XX The invention relates to Hepatitis C virus (HCV) envelope protein with N-
 CC glycosylation site(s). The HCV envelope protein, or the pharmaceutical
 CC composition comprising the envelope protein, is useful as a medicament or
 CC a vaccine, particularly for inducing a HCV-specific immune response,
 CC including HCV-specific antibodies or inducing a T-cell function in a
 CC mammal. The protein is particularly useful for preventing, treating or
 CC diagnosing HCV infection. It is also useful for detecting the presence of
 CC anti-HCV antibodies in a sample. The present sequence is Hepatitis C
 CC virus protein used in the invention
 CC
 XX Sequence 192 AA;
 SQ
 Query Match 100.0%; Score 185; DB 6; Length 192;
 Best Local Similarity 100.0%; Pred. No. 6.9e-20;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
 Db 116 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 149
 RESULT 6
 AAO18668
 ID AAO18668 standard; protein; 200 AA.
 XX
 AC AAO18668;
 XX
 XX 24-OCT-2002 (first entry)
 DT
 XX
 XX Hepatitis C virus clone HCC139 E1 protein.
 DE
 XX Hepatitis C virus; HCV; E1 protein; E2 protein; infection; virucide;
 KM immunostimulant; vaccine.
 XX
 XX Hepatitis C virus.
 OS
 XX WO200255548-A2.
 FN
 XX 18-JUL-2002.
 PD
 XX 11-JAN-2002; 2002WO-BE000219.
 PF
 XX 11-JAN-2001; 2001US-0260669P.
 PR 30-AUG-2001; 2001US-0315768P.
 XX
 XX (INNO-) INNOGENETICS NV.
 PA
 XX Maertens G, Bosman F, Buyse M;
 PI

DR MPI: 2002-599657/64.
 DR N-PSDB; AAU48927.
 XX
 PT New therapeutic vaccine compositions comprising at least one purified
 PT recombinant hepatitis C virus (HCV) single or specific oligomeric
 PT recombinant envelope protein E1 or E2, useful for immunizing humans from
 PT HCV infection.
 XX
 PS Disclosure; Page 178-179; 243pp; English.
 XX
 CC The present invention relates to new therapeutic vaccine compositions for
 CC inducing hepatitis C virus (HCV)-specific antibodies, comprising a
 CC composition containing at least one purified recombinant HCV single or
 CC specific oligomeric recombinant envelope proteins selected from an E1 and
 CC an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are
 CC useful for inducing HCV-specific antibodies or for immunising humans
 CC against HCV. The recombinant HCV E1 and/or E2 proteins are useful as
 CC vaccines or therapeutics, in HCV screening and confirmatory antibody
 CC tests, for raising antibodies, in the preparation of medicament, and for
 CC in vitro monitoring of HCV disease or prognosing the response to
 CC treatment of patients suffering from HCV infection. The present sequence
 CC is a protein described in the exemplification of the invention
 XX
 SQ Sequence 200 AA;
 Query Match 100.0%; Score 185; DB 5; Length 200;
 Best Local Similarity 100.0%; Pred. No. 7.2e-20;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STYFGHITGHRMAMDMNMWSPTTALVVSQLLRI 34
 DB 166 STYFGHITGHRMAMDMNMWSPTTALVVSQLLRI 199
 RESULT 7
 ADD55534
 ID ADD55534 standard; protein; 200 AA.
 XX
 AC ADD55534;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Hepatitis C virus E1/E2 protein #3.
 XX
 KW Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;
 KW liver fibrosis.
 XX
 OS Hepatitis C virus.
 XX
 PN WO2003051912-A2.
 PD 26-JUN-2003.
 XX
 PF 18-DEC-2002; 2002WO-EP014480.
 XX
 PR 18-DEC-2001; 2001US-00020510.
 PR 16-OCT-2002; 2002US-0418358P.
 XX
 PA (INNO-) INNOGENETICS NV.
 PA Maertens G, Depla E, Bosman F;
 PI
 XX
 DR MPI: 2003-541632/51.
 DR N-PSDB; ADD55533.
 XX
 PT New hepatitis C virus (HCV) vaccine composition, useful for reducing
 PT liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.
 XX
 PS Disclosure; SEQ ID NO 26; 271pp; English.
 CC The invention comprises an Hepatitis C virus (HCV) vaccine for reducing
 CC liver disease. The vaccine of the invention comprises an HCV E1 or E2
 CC protein as an antigen. The HCV vaccine is useful for reducing liver

CC disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The
 CC present amino acid sequence represents an HCV E1/E2 protein.
 XX
 SQ Sequence 200 AA;
 Query Match 100.0%; Score 185; DB 7; Length 200;
 Best Local Similarity 100.0%; Pred. No. 7.2e-20;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STYFGHITGHRMAMDMNMWSPTTALVVSQLLRI 34
 DB 166 STYFGHITGHRMAMDMNMWSPTTALVVSQLLRI 199
 RESULT 8
 ADP71116
 ID ADP71116 standard; protein; 200 AA.
 XX
 AC ADP71116;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE HCV E1 protein hydrophobic region I deletion mutant HCC139.
 XX
 KW Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
 KW liver disease; liver fibrosis; muten;
 KW serum alanine aminotransferase level; steatosis;
 KW anti-E2 immunoreactivity; vaccine; mutant.
 XX
 OS Hepatitis C virus.
 OS Synthetic.
 XX
 PN US2004126395-A1.
 PD 01-JUL-2004.
 XX
 PF 18-DEC-2002; 2002US-00321798.
 XX
 PR 18-DEC-2001; 2001US-0453708P.
 PR 16-OCT-2002; 2002US-0418358P.
 XX
 PA (MAER/) MAERTENS G.
 PA (DEPL/) DEPLA E.
 PA (BOSM/) BOSMAN F.
 PI Maertens G, Depla E, Bosman F;
 XX
 DR MPI: 2004-499089/47.
 DR N-PSDB; ADP71115.
 XX
 PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver
 PT disease, serum alanine aminotransferase levels, steatosis, or anti-E2
 PT immunoreactivity in the liver of a chronic HCV-infected mammal.
 XX
 PS Example 2; SEQ ID NO 26; 176pp; English.
 CC The invention relates to the use of a hepatitis C virus (HCV) vaccine
 CC composition for reducing liver disease (such as liver fibrosis or its
 CC progression), serum alanine aminotransferase (ALT) levels, steatosis, or
 CC anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,
 CC or for treating a chronic HCV-infected mammal. The liver disease is
 CC reduced by at least 1-2 points according to the overall Ishak score in
 CC the HCV-infected mammal. Also included are a method for predicting
 CC changes in liver disease in a chronic HCV-infected mammal, a therapeutic
 CC HCV vaccine composition (comprising at least one purified or a
 CC combination of at least 2 HCV single or specific oligomeric recombinant
 CC envelope protein selected from an E1 or E2 protein, a part of E1 and E2
 CC proteins, an E1/E2 protein complex formed from purified HCV single or
 CC specific oligomeric recombinant E1 or E2 proteins or its parts and
 CC optionally a pharmaceutical adjuvant), a composition (comprising at least
 CC one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant), an
 CC immunogenic HCV composition (or HCV vaccine composition) comprising a
 CC recombinant virus allowing expression of at least one HCV recombinant

CC envelope protein (selected from an E1 protein and/or an E2 protein, and
 CC their parts, and optionally, a pharmaceutical adjuvant) and an HCV
 CC vaccine composition (comprising a recombinant virus allowing expression
 CC of at least one HCV recombinant envelope protein chosen from an E1
 CC protein and/or an E2 protein, and parts of the E1 and E2 proteins and,
 CC optionally, a pharmaceutical adjuvant. The HCV vaccine composition is
 CC useful for reducing liver disease (such as liver fibrosis or its
 CC progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in
 CC the liver in a chronic HCV-infected mammal, or for treating a chronic HCV
 CC -infected mammal, particularly human. The HCV E1 proteins are useful for
 CC in vitro monitoring HCV disease or prognosing the response to treatment
 CC of patients suffering from HCV infection. The present sequence is an HCV
 CC E1 protein lacking its hydrophobic domain.

CC Sequence 200 AA;

Query Match 100.0%; Score 185; DB 8; Length 200;
 Best Local Similarity 100.0%; Pred. No. 7.7e-20;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
 DB 166 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 199

RESULT 9

AA018669 standard; protein; 210 AA.

AA018669;

24-OCT-2002 (first entry)

Hepatitis C virus clone HCC140 E1 protein.

Hepatitis C virus; HCV; E1 protein; E2 protein; infection; virucide;

immunostimulant; vaccine.

Hepatitis C virus.

WO20025548-A2.

18-JUN-2002.

11-JAN-2002; 2002WO-EP000219.

11-JAN-2001; 2001US-0260669P.

30-AUG-2001; 2001US-0315768P.

(INNO-) INNOGENETICS NV.

Maertens G, Bosman F, Buyse M;

WPI; 2002-599657/64.

N-PSDB; AAL48928.

New therapeutic vaccine compositions comprising at least one purified

recombinant hepatitis C virus (HCV) single or specific oligomeric

recombinant envelope protein E1 or E2, useful for immunizing humans from

HCV infection.

Disclosure; Page 180-181; 243pp; English.

The present invention relates to new therapeutic vaccine compositions for

inducing hepatitis C virus (HCV)-specific antibodies, comprising a

composition containing at least one purified recombinant HCV single or

specific oligomeric recombinant envelope proteins selected from an E1 and

an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are

useful for inducing HCV-specific antibodies or for immunizing humans

against HCV. The recombinant HCV E1 and/or E2 proteins are useful as

vaccines or therapeutics, in HCV screening and confirmatory antibody

tests, for raising antibodies, in the preparation of medicament, and for

in vitro monitoring of HCV disease or prognosing the response to

CC treatment of patients suffering from HCV infection. The present sequence
 CC is a protein described in the exemplification of the invention

CC Sequence 210 AA;

Query Match 100.0%; Score 185; DB 5; Length 210;
 Best Local Similarity 100.0%; Pred. No. 7.7e-20;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
 DB 166 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 199

RESULT 10

ADD5536 standard; protein; 210 AA.

ADD5536;

15-JAN-2004 (first entry)

Hepatitis C virus E1/E2 protein #4.

Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;

liver fibrosis.

Hepatitis C virus.

WO2003051912-A2.

26-JUN-2003.

18-DEC-2002; 2002WO-EP014480.

18-DEC-2001; 2001US-00020510.

16-OCT-2002; 2002US-0418358P.

(INNO-) INNOGENETICS NV.

Maertens G, Depia E, Bosman F;

WPI; 2003-541632/51.

N-PSDB; ADD5535.

New hepatitis C virus (HCV) vaccine composition, useful for reducing

liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.

Disclosure; SEQ ID NO 28; 271pp; English.

The invention comprises an Hepatitis C virus (HCV) vaccine for reducing

liver disease. The vaccine of the invention comprises an HCV E1 or E2

protein as an antigen. The HCV vaccine is useful for reducing liver

disease (e.g., liver fibrosis) in a chronic HCV-infected mammal. The

present amino acid sequence represents an HCV E1/E2 protein.

Sequence 210 AA;

Query Match 100.0%; Score 185; DB 7; Length 210;
 Best Local Similarity 100.0%; Pred. No. 7.7e-20;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
 DB 166 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 199

RESULT 11

ADP71118 standard; protein; 210 AA.

ADP71118;

DT 23-SEP-2004 (first entry)

XX HCV E1 protein hydrophobic region I deletion mutant HC140.

XX Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;

XX liver disease; liver fibrosis; steatosis; anti-E2 immunoreactivity; vaccine; mutant.

XX anti-E2 immunoreactivity; vaccine; mutant.

XX Hepatitis C virus.

XX Synthetic.

XX US2004126395-A1.

XX 01-JUL-2004.

XX 18-DEC-2002; 2002US-00321798.

XX 18-DEC-2001; 2001US-0453708P.

XX 16-OCT-2002; 2002US-0418358P.

XX (MAER/) MAERTENS G.

XX (DEPL/) DEPLA E.

XX (BOSM/) BOSMAN F.

XX Maertens G, Depla E, Bosman F;

XX WPI; 2004-499089/47.

XX N-PSDB; ADP71117.

XX Use of hepatitis C virus (HCV) vaccine composition for reducing liver

XX disease, serum alanine aminotransferase levels, steatosis, or anti-E2

XX immunoreactivity in the liver of a chronic HCV-infected mammal.

XX Example 2, SEQ ID NO 28, 176pp; English.

XX The invention relates to the use of a hepatitis C virus (HCV) vaccine

XX composition for reducing liver disease (such as liver fibrosis or its

XX progression), serum alanine aminotransferase (ALT) levels, steatosis, or

XX anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,

XX or for treating a chronic HCV-infected mammal. The liver disease is

XX reduced by at least 1-2 points according to the overall Ishak score in

XX the HCV-infected mammal. Also included are a method for predicting

XX changes in liver disease in a chronic HCV-infected mammal, a therapeutic

XX HCV vaccine composition (comprising at least one purified or a

XX combination of at least 2 HCV single or specific oligomeric recombinant

XX envelope protein selected from an E1 or E2 protein, a part of E1 and E2

XX proteins, an E1/E2 protein complex formed from purified HCV single or

XX specific oligomeric recombinant E1 or E2 proteins or its parts and

XX optionally a pharmaceutical adjuvant), a composition (comprising at least

XX one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant), an

XX immunogenic HCV composition (or HCV vaccine composition) comprising a

XX recombinant virus allowing expression of at least one HCV recombinant

XX envelope protein (selected from an E1 protein and/or an E2 protein, and

XX their parts, and optionally, a pharmaceutical adjuvant) and an HCV

XX vaccine composition (comprising a recombinant virus allowing expression

XX of at least one HCV recombinant envelope protein chosen from an E1

XX protein and/or an E2 protein, and parts of the E1 and E2 proteins and,

XX optionally, a pharmaceutical adjuvant. The HCV vaccine composition is

XX useful for reducing liver disease (such as liver fibrosis or its

XX progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in

XX the liver in a chronic HCV-infected mammal, or for treating a chronic HCV

XX infected mammal, particularly human. The HCV E1 proteins are useful for

XX in vitro monitoring HCV disease or prognosing the response to treatment

XX of patients suffering from HCV infection. The present sequence is an HCV

XX E1 protein lacking its hydrophobic domain.

XX SQ

XX Sequence 210 AA;

XX Query Match 100.0%; Score 185; DB 8; Length 210;

XX Best Local Similarity 100.0%; Pred. NO. 7.7e-20;

XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Oy      166 SIYPGHITGHRAMDMNNMNSPTTALVVSQLLRI 134
        |||||
        166 SIYPGHITGHRAMDMNNMNSPTTALVVSQLLRI 139
        |||||

RESULT 12
AA018660 ID AA018660 standard; protein; 212 AA.
XX
XX      AA018660;
AC
XX      24-OCT-2002 (first entry)
DT
XX      Hepatitis C virus clone HCC19A E1 protein.
DE
XX      Hepatitis C virus; HCV; E1 protein; E2 protein; infection; virucide;
KW      immunostimulant; vaccine.
XX      Hepatitis C virus.
OS      WO200255548-A2.
PN
XX      18-JUL-2002.
PD
XX      11-JAN-2002; 2002WO-EP000219.
PF
XX      11-JAN-2001; 2001US-0260669P.
PR      30-AUG-2001; 2001US-0315768P.
PR
XX      (INNO-) INNOGENETICS NV.
XX      Maertens G, Bosman F, Buyse M;
XX      WPI; 2002-599657/64.
XX      N-PSDB; AAL48913.
DR
XX      New therapeutic vaccine compositions comprising at least one purified
PT      recombinant hepatitis C virus (HCV) single or specific oligomeric
PT      recombinant envelope protein E1 or E2, useful for immunizing humans from
PT      HCV infection.
XX
XX      Disclosure; Page 159-160; 243pp; English.
XX
XX      The present invention relates to new therapeutic vaccine compositions for
CC      inducing hepatitis C virus (HCV)-specific antibodies, comprising a
CC      composition containing at least one purified recombinant HCV single or
CC      specific oligomeric recombinant envelope proteins selected from an E1 and
CC      an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are
CC      useful for inducing HCV-specific antibodies or for immunising humans
CC      against HCV. The recombinant HCV E1 and/or E2 proteins are useful as
CC      vaccines or therapeutics, in HCV screening and confirmatory antibody
CC      tests, for raising antibodies, in the preparation of medicament, and for
CC      in vitro monitoring of HCV disease or prognosing the response to
CC      treatment of patients suffering from HCV infection. The present sequence
CC      is a protein described in the exemplification of the invention
XX
XX      Sequence 212 AA;
SO

Query Match      100.0%; Score 185; DB 5; Length 212;
Best Local Similarity 100.0%; Prod. No. 7.7e-20;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 SIYPGHITGHRAMDMNNMNSPTTALVVSQLLRI 134
        |||||
        139 SIYPGHITGHRAMDMNNMNSPTTALVVSQLLRI 172
        |||||

RESULT 13
ADD55512 ID ADD55512 standard; protein; 212 AA.
AC      ADD55512;
XX

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DT 15-JAN-2004 (first entry)
XX Hepatitis C virus E1 protein #1.
DE Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;
XX liver fibrosis.
KW Hepatitis C virus.
OS Hepatitis C virus.
XX WO2003051912-A2.
XX 26-JUN-2003.
XX 18-DEC-2002; 2002WO-EP014480.
XX 18-DEC-2001; 2001US-00020510.
XX 16-OCT-2002; 2002US-0418358P.
XX (INNO-) INNOGENETICS NV.
XX Maertens G, Depia E, Bosman F;
XX WPI; 2003-541632/51.
XX N-PSDB; ADD55634.
XX New hepatitis C virus (HCV) vaccine composition, useful for reducing
XX liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.
XX Disclosure; SEQ ID NO 4; 271pp; English.
XX PS The invention comprises an Hepatitis C virus (HCV) vaccine for reducing
XX liver disease. The vaccine of the invention comprises an HCV E1 or E2
XX protein as an antigen. The HCV vaccine is useful for reducing liver
XX disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The
XX present amino acid sequence represents an HCV E1 protein.
XX SQ Sequence 212 AA;
XX
XX Query Match 100.0%; Score 185; DB 7; Length 212;
XX Best Local Similarity 100.0%; Pred. No. 7,7e-20;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
DB 139 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 172

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PA (MAER/) MAERTENS G.
PA (DEPL/) DEPIA E.
PA (BOSM/) BOSMAN F.
XX Maertens G, Depia E, Bosman F;
XX WPI; 2004-499089/47.
XX N-PSDB; ADP71093.
XX Use of hepatitis C virus (HCV) vaccine composition for reducing liver
XX disease, serum alanine aminotransferase levels, steatosis, or anti-E2
XX immunoreactivity in the liver of a chronic HCV-infected mammal.
XX Example 2; SEQ ID NO 4; 176pp; English.
XX PS The invention relates to the use of a hepatitis C virus (HCV) vaccine
XX composition for reducing liver disease (such as liver fibrosis or its
XX progression), serum alanine aminotransferase (ALT) levels, steatosis, or
XX anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,
XX or for treating a chronic HCV-infected mammal. The liver disease is
XX reduced by at least 1-2 points according to the overall Ishak score in
XX the HCV-infected mammal. Also included are a method for predicting
XX changes in liver disease in a chronic HCV-infected mammal, a therapeutic
XX HCV vaccine composition (comprising at least one purified or a
XX combination of at least 2 HCV single or specific oligomeric recombinant
XX envelope protein selected from an E1 or E2 protein, a part of E1 and E2
XX proteins, an E1/E2 protein complex formed from purified HCV single or
XX specific oligomeric recombinant E1 or E2 proteins or its parts and
XX optionally a pharmaceutical adjuvant), a composition (comprising at least
XX one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant), an
XX immunogenic HCV composition (or HCV vaccine composition) comprising a
XX recombinant virus allowing expression of at least one HCV recombinant
XX envelope protein (selected from an E1 protein and/or an E2 protein, and
XX their parts, and optionally, a pharmaceutical adjuvant) and an HCV
XX vaccine composition (comprising a recombinant virus allowing expression
XX of at least one HCV recombinant envelope protein chosen from an E1
XX protein and/or an E2 protein, and parts of the E1 and E2 proteins and,
XX optionally, a pharmaceutical adjuvant. The HCV vaccine composition is
XX useful for reducing liver disease (such as liver fibrosis or its
XX progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in
XX the liver in a chronic HCV-infected mammal, or for treating a chronic HCV
XX -infected mammal, particularly human. The HCV E1 proteins are useful for
XX in vitro monitoring HCV disease or prognosing the response to treatment
XX of patients suffering from HCV infection. The present sequence is an HCV
XX E1 protein (or fragment).
XX SQ Sequence 212 AA;
XX
XX Query Match 100.0%; Score 185; DB 8; Length 212;
XX Best Local Similarity 100.0%; Pred. No. 7,7e-20;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
DB 139 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 172

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RESULT 14
ADP71094
ID ADP71094 standard; protein; 212 AA.
AC ADP71094;
XX 23-SEP-2004 (first entry)
DT HCV E1 protein HCC19A.
DE
XX Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
XX liver disease; liver fibrosis; immunogen;
XX serum alanine aminotransferase level; steatosis;
XX anti-E2 immunoreactivity; vaccine.
XX Hepatitis C virus.
XX US2004126395-A1.
XX 01-JUL-2004.
XX 18-DEC-2002; 2002US-00321798.
XX 18-DEC-2001; 2001US-0453708P.
XX 16-OCT-2002; 2002US-0418358P.
XX

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PA (MAER/) MAERTENS G.
PA (DEPL/) DEPIA E.
PA (BOSM/) BOSMAN F.
XX Maertens G, Depia E, Bosman F;
XX WPI; 2004-499089/47.
XX N-PSDB; ADP71093.
XX Use of hepatitis C virus (HCV) vaccine composition for reducing liver
XX disease, serum alanine aminotransferase levels, steatosis, or anti-E2
XX immunoreactivity in the liver of a chronic HCV-infected mammal.
XX Example 2; SEQ ID NO 4; 176pp; English.
XX PS The invention relates to the use of a hepatitis C virus (HCV) vaccine
XX composition for reducing liver disease (such as liver fibrosis or its
XX progression), serum alanine aminotransferase (ALT) levels, steatosis, or
XX anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,
XX or for treating a chronic HCV-infected mammal. The liver disease is
XX reduced by at least 1-2 points according to the overall Ishak score in
XX the HCV-infected mammal. Also included are a method for predicting
XX changes in liver disease in a chronic HCV-infected mammal, a therapeutic
XX HCV vaccine composition (comprising at least one purified or a
XX combination of at least 2 HCV single or specific oligomeric recombinant
XX envelope protein selected from an E1 or E2 protein, a part of E1 and E2
XX proteins, an E1/E2 protein complex formed from purified HCV single or
XX specific oligomeric recombinant E1 or E2 proteins or its parts and
XX optionally a pharmaceutical adjuvant), a composition (comprising at least
XX one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant), an
XX immunogenic HCV composition (or HCV vaccine composition) comprising a
XX recombinant virus allowing expression of at least one HCV recombinant
XX envelope protein (selected from an E1 protein and/or an E2 protein, and
XX their parts, and optionally, a pharmaceutical adjuvant) and an HCV
XX vaccine composition (comprising a recombinant virus allowing expression
XX of at least one HCV recombinant envelope protein chosen from an E1
XX protein and/or an E2 protein, and parts of the E1 and E2 proteins and,
XX optionally, a pharmaceutical adjuvant. The HCV vaccine composition is
XX useful for reducing liver disease (such as liver fibrosis or its
XX progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in
XX the liver in a chronic HCV-infected mammal, or for treating a chronic HCV
XX -infected mammal, particularly human. The HCV E1 proteins are useful for
XX in vitro monitoring HCV disease or prognosing the response to treatment
XX of patients suffering from HCV infection. The present sequence is an HCV
XX E1 protein (or fragment).
XX SQ Sequence 212 AA;
XX
XX Query Match 100.0%; Score 185; DB 8; Length 212;
XX Best Local Similarity 100.0%; Pred. No. 7,7e-20;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
DB 139 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 172

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XX 18-JUL-2002.
PD 11-JAN-2002; 2002MO-EP000219.
XX 11-JAN-2001; 2001US-0260669P.
XX 30-AUG-2001; 2001US-0315768P.
PR 11-JAN-2001; 2001US-0260669P.
XX 30-AUG-2001; 2001US-0315768P.
PA (INNO-) INNOGENETICS NV.
XX Maertens G, Bosman F, Buyse M;
XX WPI, 2002-599657/64.
DR N-PSDB; AAL48925.
XX New therapeutic vaccine compositions comprising at least one purified
PT recombinant hepatitis C virus (HCV) single or specific oligonucleotide
PT recombinant envelope protein E1 or E2, useful for immunizing humans from
XX HCV infection.
XX Disclosure; Page 174-175; 243pp; English.
XX The present invention relates to new therapeutic vaccine compositions for
CC inducing hepatitis C virus (HCV)-specific antibodies, comprising a
CC composition containing at least one purified recombinant HCV single or
CC specific oligonucleotide recombinant envelope proteins selected from an E1 and
CC an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are
CC useful for inducing HCV-specific antibodies or for immunizing humans
CC against HCV. The recombinant HCV E1 and/or E2 proteins are useful as
CC vaccines or therapeutic, in HCV screening and confirmatory antibody
CC tests, for raising antibodies, in the preparation of medicament, and for
CC in vitro monitoring of HCV disease or prognosis. The present sequence
CC is a protein described in the exemplification of the invention
XX
SQ Sequence 239 AA;
Query Match 100.0%; Score 185; DB 5; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.9e-20;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQRLRI 34
Db 166 SIYPGHITGHRMAMDMNMWSPPTALVVSQRLRI 199
RESULT 16
ADD55530
ID ADD55530 standard; protein; 239 AA.
XX
AC ADD55530;
XX
DT 15-JAN-2004 (first entry)
XX
DE Hepatitis C virus E1/E2 protein #1.
XX
KW Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;
XX liver fibrosis.
XX
OS Hepatitis C virus.
XX
PN WO2003051912-A2.
XX
PD 26-JUN-2003.
XX
PF 18-DEC-2002; 2002MO-BP014480.
XX
PR 18-DEC-2001; 2001US-00020510.
XX 16-OCT-2002; 2002US-0418358P.
XX (INNO-) INNOGENETICS NV.
XX Maertens G, Depia E, Bosman F;

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XX WPI; 2003-541632/51.
DR N-PSDB; ADD55529.
XX
PT New hepatitis C virus (HCV) vaccine composition, useful for reducing
PT liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.
XX
XX Disclosure; SEQ ID NO 22; 271pp; English.
XX
CC The invention comprises an Hepatitis C virus (HCV) vaccine for reducing
CC liver disease. The vaccine of the invention comprises an HCV E1 or E2
CC protein as an antigen. The HCV vaccine is useful for reducing liver
CC disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The
CC present amino acid sequence represents an HCV E1/E2 protein.
XX
SQ Sequence 239 AA;
Query Match 100.0%; Score 185; DB 7; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.9e-20;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQRLRI 34
Db 166 SIYPGHITGHRMAMDMNMWSPPTALVVSQRLRI 199
RESULT 17
ADP71112
ID ADP71112 standard; protein; 239 AA.
XX
AC ADP71112;
XX
DT 23-SEP-2004 (first entry)
XX
DE HCV E1 protein hydrophobic region I deletion mutant HCC137.
XX
KW Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
XX liver disease; liver fibrosis; mucin;
XX serum alanine aminotransferase level; steatosis;
XX anti-E2 immunoreactivity; vaccine; mutant.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
PN US2004126395-A1.
XX
PD 01-JUL-2004.
XX
PF 18-DEC-2002; 2002US-00321798.
XX
PR 18-DEC-2001; 2001US-0453708P.
XX 16-OCT-2002; 2002US-0418358P.
XX
PA (MAER/) MAERTENS G.
PA (DEPL/) DEPLA E.
PA (BOSM/) BOSMAN F.
XX
PI Maertens G, Depia E, Bosman F;
XX
DR WPI; 2004-499089/47.
DR N-PSDB; ADP71111.
XX
PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver
PT disease, serum alanine aminotransferase levels, steatosis, or anti-E2
PT immunoreactivity in the liver of a chronic HCV-infected mammal.
XX
XX Example 2; SEQ ID NO 22; 176pp; English.
XX
CC The invention relates to the use of a hepatitis C virus (HCV) vaccine
CC composition for reducing liver disease (such as liver fibrosis or its
CC progression), serum alanine aminotransferase (ALT) levels, steatosis, or
CC anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,
CC or for treating a chronic HCV-infected mammal. The liver disease is

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CC reduced by at least 1-2 points according to the overall Ishak score in
 CC the HCV-infected mammal. Also included are a method for predicting
 CC changes in liver disease in a chronic HCV-infected mammal, a therapeutic
 CC HCV vaccine composition (comprising at least one purified or a
 CC combination of at least 2 HCV single or specific oligomeric recombinant
 CC envelope protein selected from an E1 or E2 protein, a part of E1 and E2
 CC proteins, an E1/E2 protein complex formed from purified HCV single or
 CC specific oligomeric recombinant E1 or E2 proteins or its parts and
 CC optionally a pharmaceutical adjuvant), a pharmaceutical adjuvant, an
 CC one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant, an
 CC immunogenic HCV composition (or HCV vaccine composition) comprising a
 CC recombinant virus allowing expression of at least one HCV recombinant
 CC envelope protein (selected from an E1 protein and/or an E2 protein, and
 CC their parts, and optionally, a pharmaceutical adjuvant) and an HCV
 CC vaccine composition (comprising a recombinant virus allowing expression
 CC of at least one HCV recombinant envelope protein chosen from an E1
 CC protein and/or an E2 protein, and parts of the E1 and E2 proteins and,
 CC optionally, a pharmaceutical adjuvant. The HCV vaccine composition is
 CC useful for reducing liver disease (such as liver fibrosis or its
 CC progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in
 CC the liver in a chronic HCV-infected mammal, or for treating a chronic HCV
 CC -infected mammal, particularly human. The HCV E1 proteins are useful for
 CC in vitro monitoring HCV disease or prognosing the response to treatment
 CC of patients suffering from HCV infection. The present sequence is an HCV
 CC E1 protein lacking its hydrophobic domain.

SQ Sequence 239 AA;

Query Match 100.0%; Score 185; DB 8; Length 239;

Best Local Similarity 100.0%; Pred. No. 8.98-20; Mismatches 0; Gaps 0;

Matches 34; Conservative 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
 |||||
 166 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 199

RESULT 18

AA018661 ID AA018661 standard; protein; 263 AA.

AC AA018661;

DT 24-OCT-2002 (first entry)

DE Hepatitis C virus clone HCC110A E1 protein.

XX Hepatitis C virus; HCV; E1 protein; E2 protein; infection; virucide;

KW immunostimulant; vaccine.

XX Hepatitis C virus.

OS Hepatitis C virus.

PN WO200255548-A2.

PD 18-JUL-2002.

PF 11-JAN-2002; 2002WO-EP000219.

PR 11-JAN-2001; 2001US-0260669P.

PS 30-AUG-2001; 2001US-0315768P.

XX (INNO-) INNOGENETICS NV.

PI Maertens G, Bosman F, Buyse M;

DR WPI; 2002-599637/64.

XX N-PSDB; AAL48914.

PT New therapeutic vaccine compositions comprising at least one purified
 PT recombinant hepatitis C virus (HCV) single or specific oligomeric
 PT recombinant envelope protein E1 or E2, useful for immunizing humans from
 PT HCV infection.

PS Disclosure; Page 162-163; 243pp; English.

XX The present invention relates to new therapeutic vaccine compositions for
 CC inducing hepatitis C virus (HCV)-specific antibodies, comprising a
 CC composition containing at least one purified recombinant HCV single or
 CC specific oligomeric recombinant envelope proteins selected from an E1 and
 CC an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are
 CC useful for inducing HCV-specific antibodies or for immunizing humans
 CC against HCV. The recombinant HCV E1 and/or E2 proteins are useful as
 CC vaccines or therapeutics, in HCV screening and confirmatory antibody
 CC tests, for raising antibodies, in the preparation of medicament, and for
 CC in vitro monitoring of HCV disease or prognosing the response to
 CC treatment of patients suffering from HCV infection. The present sequence
 CC is a protein described in the exemplification of the invention

SQ Sequence 263 AA;

Query Match 100.0%; Score 185; DB 5; Length 263;

Best Local Similarity 100.0%; Pred. No. 1e-19; Mismatches 0; Gaps 0;

Matches 34; Conservative 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
 |||||
 190 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 223

RESULT 19

ADD55514 ID ADD55514 standard; protein; 263 AA.

AC ADD55514;

DT 15-JAN-2004 (first entry)

DE Hepatitis C virus E1 protein #2.

XX Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;

KW liver fibrosis.

XX Hepatitis C virus.

PN WO2003051912-A2.

PD 26-JUN-2003.

PF 18-DEC-2002; 2002WO-EP014480.

PR 18-DEC-2001; 2001US-00020510.

PS 16-OCT-2002; 2002US-0418358P.

XX (INNO-) INNOGENETICS NV.

PI Maertens G, Depla E, Bosman F;

DR WPI; 2003-541632/51.

PS N-PSDB; ADD55513.

PT New hepatitis C virus (HCV) vaccine composition, useful for reducing
 PT liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.

XX Disclosure; SEQ ID NO 6; 27pp; English.

XX The invention comprises an Hepatitis C virus (HCV) vaccine for reducing
 CC liver disease. The vaccine of the invention comprises an HCV E1 or E2
 CC protein as an antigen. The HCV vaccine is useful for reducing liver
 CC disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The
 CC present amino acid sequence represents an HCV E1 protein.

SQ Sequence 263 AA;

Query Match 100.0%; Score 185; DB 7; Length 263;

Best Local Similarity 100.0%; Pred. No. 1e-19; Mismatches 0; Gaps 0;

Matches 34; Conservative 0; Indels 0; Gaps 0;

QY 1 STYPGHITGRMAMDMNMWSPPTALVVSQLLRI 34
 DB 190 STYPGHITGRMAMDMNMWSPPTALVVSQLLRI 223

RESULT 20
 ADP71096
 ID ADP71096 standard; protein; 263 AA.

AC ADP71096;
 DT 23-SEP-2004 (first entry)
 XX HCV E1 protein HCC110A.

XX Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
 KM liver disease; liver fibrosis; immunogen;
 KM serum alanine aminotransferase level; steatosis;
 KM anti-E2 immunoreactivity; vaccine.

OS Hepatitis C virus.
 XX US2004126395-A1.

PN 01-JUL-2004.

XX 18-DEC-2002; 2002US-00321738.

PR 18-DEC-2001; 2001US-0453708P.
 PR 16-OCT-2002; 2002US-0418358P.

PA (MAER/) MAERTENS G.
 PA (DEPL/) DEPLA E.
 PA (BOSM/) BOSMAN F.

XX Maertens G, Depia E, Bosman F;

PI WPI; 2004-499089/47.
 DR N-PSDB; ADP71095.

PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver
 PT disease, serum alanine aminotransferase levels, steatosis, or anti-E2
 PT immunoreactivity in the liver of a chronic HCV-infected mammal.

XX Example 2; SEQ ID NO 6; 176pp; English.

XX The invention relates to the use of a hepatitis C virus (HCV) vaccine
 CC composition for reducing liver disease (such as liver fibrosis or its
 CC progression), serum alanine aminotransferase (ALT) levels, steatosis, or
 CC anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,
 CC or for treating a chronic HCV-infected mammal. The liver disease is
 CC reduced by at least 1-2 points according to the overall Ishak score in
 CC the HCV-infected mammal. Also included are a method for predicting
 CC changes in liver disease in a chronic HCV-infected mammal, a therapeutic
 CC HCV vaccine composition (comprising at least one purified or a
 CC combination of at least 2 HCV single or specific oligomeric recombinant
 CC envelope protein selected from an E1 or E2 protein, a part of E1 and E2
 CC proteins, an E1/E2 protein complex formed from purified HCV single or
 CC specific oligomeric recombinant E1 or E2 proteins or its parts and
 CC optionally a pharmaceutical adjuvant), a composition (comprising at least
 CC one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant), an
 CC immunogenic HCV composition (or HCV vaccine composition) comprising a
 CC recombinant virus allowing expression of at least one HCV recombinant
 CC envelope protein (selected from an E1 protein and/or an E2 protein, and
 CC their parts, and optionally, a pharmaceutical adjuvant) and an HCV
 CC vaccine composition (comprising a recombinant virus allowing expression
 CC of at least one HCV recombinant envelope protein chosen from an E1
 CC protein and/or an E2 protein, and parts of the E1 and E2 proteins and,
 CC optionally, a pharmaceutical adjuvant. The HCV vaccine composition is
 CC useful for reducing liver disease (such as liver fibrosis or its
 CC progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in
 CC the liver in a chronic HCV-infected mammal, or for treating a chronic HCV

CC -infected mammal, particularly human. The HCV E1 proteins are useful for
 CC in vitro monitoring HCV disease or diagnosing the response to treatment
 CC of patients suffering from HCV infection. The present sequence is an HCV
 CC E1 protein (or fragment).

XX Sequence 263 AA;

Query Match 100.0%; Score 185; DB 8; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1e-19;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYPGHITGRMAMDMNMWSPPTALVVSQLLRI 34
 DB 190 STYPGHITGRMAMDMNMWSPPTALVVSQLLRI 223

RESULT 21
 AAO18678
 ID AAO18678 standard; protein; 692 AA.

AC AAO18678;

DT 24-OCT-2002 (first entry)

DE Hepatitis C virus E2 protein related protein SEQ ID NO: 48.

KM Hepatitis C virus; HCV; E1 protein; E2 protein; infection; vaccine;
 KM immunostimulant; vaccine.

OS Hepatitis C virus.

PN WO200255548-A2.

PD 18-JUL-2002.

PF 11-JAN-2002; 2002WO-EP000219.

PR 11-JAN-2001; 2001US-0260669P.
 PR 30-AUG-2001; 2001US-0315768P.

PA (INNO-) INNOGENETICS NV.

PI Maertens G, Bosman F, Buysse M;

DR WPI; 2002-599657/64.
 DR N-PSDB; AAL48939.

PT New therapeutic vaccine compositions comprising at least one purified
 PT recombinant hepatitis C virus (HCV) single or specific oligomeric
 PT recombinant envelope protein E1 or E2, useful for immunizing humans from
 PT HCV infection.

XX Disclosure; Page 209-211; 243pp; English.

XX The present invention relates to new therapeutic vaccine compositions for
 CC inducing hepatitis C virus (HCV)-specific antibodies, comprising a
 CC composition containing at least one purified recombinant HCV single or
 CC specific oligomeric recombinant envelope proteins selected from an E1 and
 CC an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are
 CC useful for inducing HCV-specific antibodies or for immunizing humans
 CC against HCV. The recombinant HCV E1 and/or E2 proteins are useful as
 CC vaccines or therapeutics, in HCV screening and confirmatory antibody
 CC tests, for raising antibodies, in the preparation of medicament, and for
 CC in vitro monitoring of HCV disease or diagnosing the response to
 CC treatment of patients suffering from HCV infection. The present sequence
 CC is a protein described in the exemplification of the invention

XX Sequence 692 AA;

Query Match 100.0%; Score 185; DB 5; Length 692;
 Best Local Similarity 100.0%; Pred. No. 3.1e-15;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
 |||||
 Db 190 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 223

RESULT 22

ADD55556
 ID ADD55556 standard; protein; 692 AA.
 AC ADD55556;
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX Hepatitis C virus E1/E2 protein #13.
 DE Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;
 XX
 XX Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;
 KW liver fibrosis.
 KM
 XX Hepatitis C virus.
 OS
 XX WO2003051912-A2.
 FN
 XX 26-JUN-2003.
 PD
 XX 18-DEC-2002; 2002MO-EP014480.
 PF
 XX 18-DEC-2001; 2001US-00020510.
 PR 16-OCT-2002; 2002US-0418358P.
 XX
 XX (INNO-) INNOGENETICS NV.
 PA
 XX Maertens G, Depla E, Bosman F;
 PI
 XX WPI, 2003-541632/51.
 DR N-PSDB; ADD55555.
 XX
 XX New hepatitis C virus (HCV) vaccine composition, useful for reducing
 PT liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.
 CC
 XX Disclosure; SEQ ID NO 48; 271pp; English.
 PS
 XX The invention comprises an Hepatitis C virus (HCV) vaccine for reducing
 CC liver disease. The vaccine of the invention comprises an HCV E1 or E2
 CC protein as an antigen. The HCV vaccine is useful for reducing liver
 CC disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The
 CC present amino acid sequence represents an HCV E1/E2 protein.
 CC
 XX Sequence 692 AA;
 SQ

Query Match 100.0%; Score 185; DB 7; Length 692;
 Best Local Similarity 100.0%; Pred. No. 3.1e-19;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
 |||||
 Db 190 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 223

RESULT 23
 ADP71138
 ID ADP71138 standard; protein; 692 AA.
 AC ADP71138;
 XX
 XX 23-SEP-2004 (first entry)
 DT
 XX HCV E1 protein HCC165.
 DE
 XX Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
 KW liver disease; liver fibrosis; immunogen;
 KM serum alanine aminotransferase level; steatosis;
 KM anti-E2 immunoreactivity; vaccine.
 XX

OS Hepatitis C virus.

FN US2004126395-A1.

XX 01-JUL-2004.

XX 18-DEC-2002; 2002US-00321798.

PR 18-DEC-2001; 2001US-0453708P.

PR 16-OCT-2002; 2002US-0418358P.

XX (MAER/) MAERTENS G.

PA (DEPL/) DEPLA E.

PA (BOSM/) BOSMAN F.

PI Maertens G, Depla E, Bosman F;

XX WPI, 2004-499089/47.

DR N-PSDB; ADP71137.

XX

PS Disclosure; SEQ ID NO 48; 176pp; English.

XX

CC The invention relates to the use of a hepatitis C virus (HCV) vaccine

CC composition for reducing liver disease (such as liver fibrosis or its

CC progression), serum alanine aminotransferase (ALT) levels, steatosis, or

CC anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,

CC or for treating a chronic HCV-infected mammal. The liver disease is

CC reduced by at least 1-2 points according to the overall Ishak score in

CC the HCV-infected mammal. Also included are a method for predicting

CC changes in liver disease in a chronic HCV-infected mammal, a therapeutic

CC HCV vaccine composition (comprising at least one purified or a

CC combination of at least 2 HCV single or specific oligomeric recombinant

CC envelope protein selected from an E1 or E2 protein, a part of E1 and E2

CC proteins, an E1/E2 protein complex formed from purified HCV single or

CC specific oligomeric recombinant E1 or E2 proteins or its parts and

CC optionally a pharmaceutical adjuvant), a composition (comprising at least

CC one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant) comprising

CC immunogenic HCV composition (or HCV vaccine composition) comprising a

CC recombinant virus allowing expression of at least one HCV recombinant

CC envelope protein (selected from an E1 protein and/or an E2 protein, and

CC their parts, and optionally, a pharmaceutical adjuvant) and an HCV

CC vaccine composition (comprising a recombinant virus allowing expression

CC of at least one HCV recombinant envelope protein chosen from an E1

CC protein and/or an E2 protein, and parts of the E1 and E2 proteins and,

CC optionally, a pharmaceutical adjuvant. The HCV vaccine composition is

CC useful for reducing liver disease (such as liver fibrosis or its

CC progression), serum ALT levels, steatosis, or for treating a chronic HCV

CC infected mammal, particularly human. The HCV E1 proteins are useful for

CC in vitro monitoring HCV disease or diagnosing the response to treatment

CC of patients suffering from HCV infection. The present sequence is an HCV

CC E1 protein (or fragment).

CC

SQ Sequence 692 AA;

XX

Query Match 100.0%; Score 185; DB 8; Length 692;
 Best Local Similarity 100.0%; Pred. No. 3.1e-19;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
 |||||
 Db 190 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 223

RESULT 24
 AAO18679
 ID AAO18679 standard; protein; 809 AA.
 AC AAO18679;

```
XX 24-OCT-2002 (first entry)
XX
XX Hepatitis C virus E2 protein related protein SEQ ID NO: 50.
DE
XX Hepatitis C virus; HCV; E1 protein; E2 protein; infection; virucide;
XX Immunostimulant; vaccine.
XX
XX Hepatitis C virus.
OS
XX WO200255548-A2.
XX
XX 18-JUL-2002.
XX
XX 11-JAN-2002; 2002WO-EP000219.
XX
XX 11-JAN-2001; 2001US-0260669P.
XX 30-AUG-2001; 2001US-0315768P.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Maertens G, Bosman F, Buyse M;
XX
XX WPI; 2002-599657/64.
XX
XX N-PSDB; AAL48940.
XX
XX New therapeutic vaccine compositions comprising at least one purified
XX recombinant hepatitis C virus (HCV) single or specific oligomeric
XX recombinant envelope protein E1 or E2, useful for immunizing humans from
XX HCV infection.
XX
XX Disclosure; Page 215-218; 243pp; English.
XX
XX The present invention relates to new therapeutic vaccine compositions for
XX inducing hepatitis C virus (HCV)-specific antibodies, comprising a
XX composition containing at least one purified recombinant HCV single or
XX specific oligomeric recombinant envelope proteins selected from an E1 and
XX an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are
XX useful for inducing HCV-specific antibodies or for immunising humans
XX against HCV. The recombinant HCV E1 and/or E2 proteins are useful as
XX vaccines or therapeutics, in HCV screening and confirmatory antibody
XX tests, for raising antibodies, in the preparation of medicament, and for
XX in vitro monitoring of HCV disease or prognosing the response to
XX treatment of patients suffering from HCV infection. The present sequence
XX is a protein described in the exemplification of the invention
XX
XX Sequence 809 AA;
SQ
XX
XX Query Match 100.0%; Score 185; DB 5; Length 809;
XX Best Local Similarity 100.0%; Pred. No. 3,7e-19;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMAMDMNMWSPPTLALVVSQLLRI 34
XX |||||
XX 307 SIYPGHITGHRMAMDMNMWSPPTLALVVSQLLRI 340
Db
XX
XX RESULT 25
XX ADD55558
XX ID ADD55558 standard; protein; 809 AA.
XX
XX ADD55558;
XX
XX 15-JAN-2004 (first entry)
XX
XX Hepatitis C virus E1/E2 protein #14.
DE
XX Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;
XX liver fibrosis.
XX
XX Hepatitis C virus.
OS
XX WO2003051912-A2.
XX
XX
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```
XX 26-JUN-2003.
XX
XX 18-DEC-2002; 2002WO-EP014480.
XX
XX 18-DEC-2001; 2001US-00020510.
XX 16-OCT-2002; 2002US-0418358P.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Maertens G, Depla E, Bosman F;
XX
XX WPI; 2003-541632/51.
XX
XX N-PSDB; ADD55557.
XX
XX New hepatitis C virus (HCV) vaccine composition, useful for reducing
XX liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.
XX
XX Disclosure; SEQ ID NO 50; 271pp; English.
XX
XX The invention comprises an Hepatitis C virus (HCV) vaccine for reducing
XX liver disease. The vaccine of the invention comprises an HCV E1 or E2
XX protein as an antigen. The HCV vaccine is useful for reducing liver
XX disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The
XX present amino acid sequence represents an HCV E1/E2 protein.
XX
XX Sequence 809 AA;
SQ
XX
XX Query Match 100.0%; Score 185; DB 7; Length 809;
XX Best Local Similarity 100.0%; Pred. No. 3,7e-19;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMAMDMNMWSPPTLALVVSQLLRI 34
XX |||||
XX 307 SIYPGHITGHRMAMDMNMWSPPTLALVVSQLLRI 340
Db
XX
XX RESULT 26
XX ADP71140
XX ID ADP71140 standard; protein; 809 AA.
XX
XX ADP71140;
XX
XX 23-SEP-2004 (first entry)
XX
XX HCV E1 protein HCC166.
XX
XX Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;
XX liver disease; liver fibrosis; immunogen;
XX serum alanine aminotransferase level; steatosis;
XX anti-E2 immunoreactivity; vaccine.
XX
XX Hepatitis C virus.
OS
XX US2004126395-A1.
XX
XX 01-JUL-2004.
XX
XX 18-DEC-2002; 2002US-00321798.
XX
XX 18-DEC-2001; 2001US-0453708P.
XX 16-OCT-2002; 2002US-0418358P.
XX
XX (MAER/) MAERTENS G.
XX (DEPL/) DEPLA E.
XX (BOSM/) BOSMAN F.
XX
XX Maertens G, Depla E, Bosman F;
XX
XX WPI; 2004-499089/47.
XX
XX N-PSDB; ADP71139.
XX
XX Use of hepatitis C virus (HCV) vaccine composition for reducing liver
XX
```

PT disease, serum alanine aminotransferase levels, steatosis, or anti-E2
PT immunoreactivity in the liver of a chronic HCV-infected mammal.
PS Disclosure; SEQ ID NO 50; 176pp; English.
XX
CC The invention relates to the use of a hepatitis C virus (HCV) vaccine
CC composition for reducing liver disease (such as liver fibrosis or its
CC progression), serum alanine aminotransferase (ALT) levels, steatosis, or
CC anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,
CC or for treating a chronic HCV-infected mammal. The liver disease is
CC reduced by at least 1-2 points according to the overall Ishak score in
CC the HCV-infected mammal. Also included are a method for predicting
CC changes in liver disease in a chronic HCV-infected mammal, a therapeutic
CC HCV vaccine composition (comprising at least one purified or a
CC combination of at least 2 HCV single or specific oligomeric recombinant
CC envelope protein selected from an E1 or E2 protein, a part of E1 and E2
CC proteins, an E1/E2 protein complex formed from purified HCV single or
CC specific oligomeric recombinant E1 or E2 proteins or its parts and
CC optionally a pharmaceutical adjuvant), a composition (comprising at least
CC one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant), an
CC immunogenic HCV composition (or HCV vaccine composition) comprising a
CC recombinant virus allowing expression of at least one HCV recombinant
CC envelope protein (selected from an E1 protein and/or an E2 protein, and
CC their parts, and optionally, a pharmaceutical adjuvant) and an HCV
CC vaccine composition (comprising a recombinant virus allowing expression
CC of at least one HCV recombinant envelope protein chosen from an E1
CC protein and/or an E2 protein, and parts of the E1 and E2 proteins and,
CC optionally, a pharmaceutical adjuvant). The HCV vaccine composition is
CC useful for reducing liver disease (such as liver fibrosis or its
CC progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in
CC the liver in a chronic HCV-infected mammal, or for treating a chronic HCV
CC -infected mammal, particularly human. The HCV E1 proteins are useful for
CC in vitro monitoring HCV disease or prognosing the response to treatment
CC of patients suffering from HCV infection. The present sequence is an HCV
CC E1 protein (or fragment).
XX
SQ Sequence 809 AA;

Query Match 100.0%; Score 185; DB 8; Length 809;
Best Local Similarity 100.0%; Pred. No. 3.7e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWMSPTTALVVSQQLRI 34
DB 307 SIYPGHITGHRMAMDMNMWMSPTTALVVSQQLRI 340

RESULT 27
AAR69647
ID AAR69647 standard; protein; 192 AA.
XX
AC AAR69647;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1995 (first entry)
XX
DE Hepatitis C virus envelope 1 protein isolate HK5.
XX
KW Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate HK5;
XX diagnosis; vaccines; antibodies; antisera; gene inhibition.
XX
OS Hepatitis C virus.
XX
PN WO9501442-A2.
XX
PD 12-JAN-1995.
XX
PF 28-JUN-1994; 94WO-US007320.
XX
PR 29-JUN-1993; 93US-00086428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX

PI Bukh J, Miller RH, Purcell RH;
XX
DR WPI; 1995-061006/08.
DR N-PSDB; AAO83859.
XX
PT Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
PT nucleotide(s), peptide(s) and proteins, used in diagnosis and in
PT vaccines.
XX
PS Claim 3; Page 90; 186pp; English.
XX
CC AAO83858 encodes AAR69647 hepatitis C virus (HCV) envelope 1 (E1) protein
CC isolate HK5, both can be used for the diagnosis of HCV infection, and in
CC the prodn. of anti-HCV vaccines, antibodies and antisera. The cDNA may
CC also be used to inhibit the expression of the HCV E1 gene. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 192 AA;

Query Match 99.5%; Score 184; DB 2; Length 192;
Best Local Similarity 97.1%; Pred. No. 9.8e-20;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWMSPTTALVVSQQLRI 34
DB 116 SIYPGHITGHRMAMDMNMWMSPTTALVVSQQLRI 149

RESULT 28
AAR69652
ID AAR69652 standard; protein; 192 AA.
XX
AC AAR69652;
XX
DT 25-MAR-2003 (revised)
DT 18-SEP-1995 (first entry)
XX
DE Hepatitis C virus envelope 1 protein isolate S9.
XX
KW Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate S9;
XX diagnosis; vaccines; antibodies; antisera; gene inhibition.
XX
OS Hepatitis C virus.
XX
PN WO9501442-A2.
XX
PD 12-JAN-1995.
XX
PF 28-JUN-1994; 94WO-US007320.
XX
PR 29-JUN-1993; 93US-00086428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
DT Bukh J, Miller RH, Purcell RH;
XX
DR WPI; 1995-061006/08.
DR N-PSDB; AAO83863.
XX
PT Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
PT nucleotide(s), peptide(s) and proteins, used in diagnosis and in
PT vaccines.
XX
PS Claim 3; Page 94; 186pp; English.
XX
CC AAO83863 encodes AAR69652 hepatitis C virus (HCV) envelope 1 (E1) protein
CC isolate S9, both can be used for the diagnosis of HCV infection, and in
CC the prodn. of anti-HCV vaccines, antibodies and antisera. The cDNA may
CC also be used to inhibit the expression of the HCV E1 gene. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 192 AA;

Query Match 99.5%; Score 184; DB 2; Length 192;
 Best Local Similarity 97.1%; Pred. No. 9.8e-20;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34
 DB 116 STYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 149

RESULT 29
 AAR69656
 ID AAR69656 standard; protein; 192 AA.
 XX AAR69656;
 AC AAR69656;
 XX AAR69656;
 DT 25-MAR-2003 (revised)
 DT 18-SEP-1995 (first entry)
 XX

DE Hepatitis C virus envelope 1 protein isolate T3.

KW Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate T3;
 KW diagnosis; vaccines; antibodies; antisera; gene inhibition.

OS Hepatitis C virus.

PN WO9501442-A2.

XX 12-JAN-1995.

XX 28-JUN-1994; 94WO-US007320.

XX 29-JUN-1993; 93US-00086428.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Bukh J, Miller RH, Purcell RH;

XX WPI; 1995-061006/08.

XX N-PSDB; AAR69656.

XX Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-nucleotide(s), peptide(s) and proteins, used in diagnosis and in vaccines.

XX Claim 3; Page 97; 186pp; English.

CC AAQ83867 encodes AAR69656 hepatitis C virus (HCV) envelope 1 (E1) protein isolate T3, both can be used for the diagnosis of HCV infection, and in the prodn. of anti-HCV vaccines, antibodies and antisera. The cDNA may also be used to inhibit the expression of the HCV E1 gene. (Updated on 25 -MAR-2003 to correct PN field.)
 CC
 CC
 CC

XX Sequence 192 AA;

Query Match 99.5%; Score 184; DB 2; Length 192;
 Best Local Similarity 97.1%; Pred. No. 9.8e-20;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34
 DB 116 STYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 149

RESULT 30
 AAR69642
 ID AAR69642 standard; protein; 192 AA.
 XX AAR69642;
 AC AAR69642;
 XX AAR69642;
 DT 25-MAR-2003 (revised)
 DT 14-SEP-1995 (first entry)
 XX

DE Hepatitis C virus envelope 1 protein isolate D1.

XX Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate D1;
 KW diagnosis; vaccines; antibodies; antisera; gene inhibition.

OS Hepatitis C virus.

PN WO9501442-A2.

XX 12-JAN-1995.

XX 28-JUN-1994; 94WO-US007320.

XX 29-JUN-1993; 93US-00086428.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Bukh J, Miller RH, Purcell RH;

XX WPI; 1995-061006/08.

XX N-PSDB; AAR69653.

XX Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-nucleotide(s), peptide(s) and proteins, used in diagnosis and in vaccines.

XX Claim 3; Page 86; 186pp; English.

CC AAQ83853 encodes AAR69642 hepatitis C virus (HCV) envelope 1 (E1) protein isolate D1, both can be used for the diagnosis of HCV infection, and in the prodn. of anti-HCV vaccines, antibodies and antisera. The cDNA may also be used to inhibit the expression of the HCV E1 gene. (Updated on 25 -MAR-2003 to correct PN field.)
 CC
 CC
 CC

XX Sequence 192 AA;

Query Match 99.5%; Score 184; DB 2; Length 192;
 Best Local Similarity 97.1%; Pred. No. 9.8e-20;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34
 DB 116 STYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 149

RESULT 31
 AAR89513
 ID AAR89513 standard; protein; 192 AA.
 XX AAR89513;
 AC AAR89513;
 XX AAR89513;
 DT 30-SEP-1996 (first entry)
 XX

DE Hepatitis C virus isolate D1 envelope 1 protein.

KW HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
 KW hepatitis.

OS Hepatitis C virus.

PN WO9605315-A2.

XX 22-FEB-1996.

XX 15-AUG-1995; 95WO-US010398.

XX 15-AUG-1994; 94US-00290665.

XX (USSH) US SEC DEPT HEALTH.

XX Bukh J, Miller RH, Purcell RH;

XX WPI; 1996-139709/14.

XX N-PSDB; AAT16567.

```

XX DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
PT determine HCV genotype and as vaccines against HCV infection.
XX
XX Claim 2; Page 116; 340bp; English.
XX
XX AAR89505-R89555 are HCV E1 (envelope-1) proteins derived from 51 HCV
CC isolates. Isolated cDNA sequences are used for the prodn. of primers
CC useful for detecting the presence of HCV in a sample, the primers are
CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
CC in vaccines for immunising against HCV infection. The proteins may also
CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
CC other mononuclear cells. The antibodies may be used in the prevention of
CC HCV infection
CC
XX Sequence 192 AA;
SQ
Query Match          99.5%; Score 184; DB 2; Length 192;
Best Local Similarity 97.1%; Pred. No. 9.8e-20;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNNMNSPTTALVVSQLLRI 34
Db 116 SIYPGHVTHGRMAMDMNNMNSPTTALVVSQLLRI 149

RESULT 32
AAR89523
ID AAR89523 standard; protein; 192 AA.
XX
AC AAR89523;
XX
DT 30-SEP-1996 (first entry)
XX
DE Hepatitis C virus isolate S9 envelope 1 protein.
XX
KW HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
KW hepatitis.
XX
OS Hepatitis C virus.
XX
PN WO9605315-A2.
XX
PD 22-FEB-1996.
XX
PF 15-AUG-1995; 95WO-US010398.
XX
PR 15-AUG-1994; 94US-00290665.
XX
PA (USSH ) US SEC DEPT HEALTH.
XX
PI Bukh J, Miller RH, Purcell RH;
XX
DR WPI; 1996-139709/14.
XX
N-PSDB; AAT16581.
XX
PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
PT determine HCV genotype and as vaccines against HCV infection.
XX
XX Claim 2; Page 124; 340bp; English.
XX
XX AAR89505-R89555 are HCV E1 (envelope-1) proteins derived from 51 HCV
CC isolates. Isolated cDNA sequences are used for the prodn. of primers
CC useful for detecting the presence of HCV in a sample, the primers are
CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
CC in vaccines for immunising against HCV infection. The proteins may also
CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
CC other mononuclear cells. The antibodies may be used in the prevention of
CC HCV infection
CC
XX Sequence 192 AA;
SQ
Query Match          99.5%; Score 184; DB 2; Length 192;
Best Local Similarity 97.1%; Pred. No. 9.8e-20;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Best Local Similarity 97.1%; Pred. No. 9.8e-20;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNNMNSPTTALVVSQLLRI 34
Db 116 SIYPGHVTHGRMAMDMNNMNSPTTALVVSQLLRI 149

RESULT 33
AAR89527
ID AAR89527 standard; protein; 192 AA.
XX
AC AAR89527;
XX
DT 30-SEP-1996 (first entry)
XX
DE Hepatitis C virus isolate T3 envelope 1 protein.
XX
KW HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
KW hepatitis.
XX
OS Hepatitis C virus.
XX
PN WO9605315-A2.
XX
PD 22-FEB-1996.
XX
PF 15-AUG-1995; 95WO-US010398.
XX
PR 15-AUG-1994; 94US-00290665.
XX
PA (USSH ) US SEC DEPT HEALTH.
XX
PI Bukh J, Miller RH, Purcell RH;
XX
DR WPI; 1996-139709/14.
XX
N-PSDB; AAT16581.
XX
PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
PT determine HCV genotype and as vaccines against HCV infection.
XX
XX Claim 2; Page 127; 340bp; English.
XX
XX AAR89505-R89555 are HCV E1 (envelope-1) proteins derived from 51 HCV
CC isolates. Isolated cDNA sequences are used for the prodn. of primers
CC useful for detecting the presence of HCV in a sample, the primers are
CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
CC in vaccines for immunising against HCV infection. The proteins may also
CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
CC other mononuclear cells. The antibodies may be used in the prevention of
CC HCV infection
CC
XX Sequence 192 AA;
SQ
Query Match          99.5%; Score 184; DB 2; Length 192;
Best Local Similarity 97.1%; Pred. No. 9.8e-20;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNNMNSPTTALVVSQLLRI 34
Db 116 SIYPGHVTHGRMAMDMNNMNSPTTALVVSQLLRI 149

RESULT 34
AAR89518
ID AAR89518 standard; protein; 192 AA.
XX
AC AAR89518;
XX
DT 30-SEP-1996 (first entry)
XX
DE Hepatitis C virus isolate HK5 envelope 1 protein.
XX

```

KM HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
 KM hepatitis.
 XX Hepatitis C virus.
 OS Hepatitis C virus.
 XX MO9605315-A2.
 PN 22-FEB-1996.
 PD 15-AUG-1995; 95WO-US010398.
 PF 15-AUG-1995; 94US-00290665.
 PR 15-AUG-1994; 94US-00290665.
 XX (USSH) US SEC DEPT HEALTH.
 XX Buxh J, Miller RH, Purcell RH;
 PI WPI; 1996-139709/14.
 DR N-PSDB; AAT16572.
 XX DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
 PT determine HCV genotype and as vaccines against HCV infection.
 CC Claim 2; Page 120; 340pp; English.
 PS AAR89505-R89555 are HCV E1 (envelope-1) proteins derived from 51 HCV
 CC isolates. Isolated cDNA sequences are used for the prodn. of primers
 CC useful for detecting the presence of HCV in a sample, the primers are
 CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
 CC in vaccines for immunising against HCV infection. The proteins may also
 CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
 CC other mononuclear cells. The antibodies may be used in the prevention of
 CC HCV infection.
 XX Sequence 192 AA;
 SQ
 Query Match 99.5%; Score 184; DB 2; Length 192;
 Best Local Similarity 97.1%; Pred. No. 9.8e-20;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYPGHITGHRAMWDMNMSPPTALVVSQRLRI 34
 DB 116 SIYPGHITGHRAMWDMNMSPPTALVVSQRLRI 149

RESULT 35
 AAB18532
 ID AAB18532 standard; protein; 106 AA.
 XX AAB18532;
 AC 15-JUN-2001 (first entry)
 DT Protein encoded by a novel hepatitis C virus cDNA clone CA156e.
 XX Hepatitis C virus; HCV, antisense polynucleotide; polyprotein;
 KM viral infectivity; viral replication.
 XX Hepatitis C virus.
 OS EP1034785-A2.
 PN 13-SEP-2000.
 PD 16-MAR-1990; 2000EP-00109602.
 PF 17-MAR-1989; 89US-00325338.
 PR 20-APR-1989; 89US-00341334.
 PR 18-MAY-1989; 89US-00355002.
 PR 16-MAR-1990; 90EP-00302866.
 XX (CHIR) CHIRON CORP.
 PA
 XX

PI Houghton M, Choo Q, Kuo G;
 XX WPI; 2000-566891/53.
 DR N-PSDB; AA75288.
 XX Novel composition comprising a hepatitis C virus antisense polynucleotide
 PT which is complementary to or corresponds to a sense strand of the virus
 PT genome, and selectively hybridizes to it.
 XX Example; Fig 8; 75pp; English.
 PS The specification describes a pharmaceutical composition which comprises
 CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
 CC characterized by a positive stranded RNA genome which has 40% homology at
 CC the polypeptide level to a HCV polypeptide. The antisense polynucleotide
 CC binds to cellular polynucleotides which enhance and/or are required for
 CC viral infectivity, replicative ability or chronicity. The antisense
 CC polynucleotides may also be designed to bind with high specificity, to be
 CC of increased stability, to be stable and to have low toxicity. The
 CC composition also comprises an agent which causes viral RNA to be
 CC inactive. The composition is used for preventing HCV replication in a
 CC system. The present sequence is encoded by a novel HCV cDNA sequence,
 CC which is used in the course of the invention.
 XX Sequence 106 AA;
 SQ
 Query Match 98.4%; Score 182; DB 3; Length 106;
 Best Local Similarity 97.1%; Pred. No. 9.9e-20;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIYPGHITGHRAMWDMNMSPPTALVVSQRLRI 34
 DB 70 SIYPGHITGHRAMWDMNMSPPTALVVSQRLRI 103

RESULT 36
 ADN35960
 ID ADN35960 standard; protein; 106 AA.
 XX ADN35960;
 AC 17-JUN-2004 (first entry)
 DT HCV cDNA clone CA156e protein.
 XX Antiviral; Vaccine; hepatitis C virus infection; HCV infection.
 KM Hepatitis C virus.
 OS EP1394255-A2.
 PN 03-MAR-2004.
 PD 16-MAR-1990; 2003EP-00016585.
 PF 17-MAR-1989; 89US-00325338.
 PR 20-APR-1989; 89US-00341334.
 PR 18-MAY-1989; 89US-00355002.
 PR 16-MAR-1990; 90EP-00302866.
 XX (CHIR) CHIRON CORP.
 PA Houghton M, Choo Q, Kuo G;
 XX WPI; 2004-193149/19.
 DR N-PSDB; ADN35961.
 XX Novel purified hepatitis C virus polypeptide comprising epitope encoded
 PT by hepatitis C virus cDNA, useful as vaccine for treating hepatitis C
 PT virus.
 XX Example 1; Fig 8; 79pp; English.
 PS

CC The present invention relates to hepatitis C virus (HCV) proteins and
 CC cDNA sequences. The sequences are useful in immunoassays for detecting
 CC antibodies directed against HCV antigen; preparing host cells transformed
 CC with a recombinant polynucleotide; screening antiviral agents and
 CC determining the effect of antiviral agent in inhibiting viral replication
 CC in cell culture system; and developing vaccine for treating HCV
 CC infection.

CC Sequence 106 AA;

Query Match 98.4%; Score 182; DB 8; Length 106;
 Best Local Similarity 97.1%; Pred. No. 9, 9e-20;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 34
 DB 70 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 103

RESULT 37

ID AAR69638 standard; protein; 192 AA.

XX AAR69638;

DT 25-MAR-2003 (revised)

DT 14-SEP-1995 (first entry)

DE Hepatitis C virus envelope 1 protein isolate S14.

KM Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate S14;

XX diagnosis; vaccines; antibodies; antisera; gene inhibition.

OS Hepatitis C virus.

XX WO9501442-A2.

XX 12-JAN-1995.

PF 28-JUN-1994; 94WO-US007320.

PR 29-JUN-1993; 93US-00086428.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Bukh J, Miller RH, Purcell RH;

DR WPI; 1995-061006/08.

DR N-PSDB; AAQ83849.

PT Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
 PT nucleotide(s), peptide(s) and proteins, used in diagnosis and in
 PT vaccines.

PS Claim 3; Page 83; 186pp; English.

CC AAQ83849 encodes AAR69638 hepatitis C virus (HCV) envelope 1 (E1) protein
 CC isolate S14, both can be used for the diagnosis of HCV infection, and in
 CC the prodn. of anti-HCV vaccines, antibodies and antisera. The cDNA may
 CC also be used to inhibit the expression of the HCV E1 gene. (Updated on 25
 CC -MAR-2003 to correct PN field.)

CC Sequence 192 AA;

Query Match 98.4%; Score 182; DB 2; Length 192;
 Best Local Similarity 97.1%; Pred. No. 2e-19;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 34
 DB 116 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 149

RESULT 38

ID AAR69640 standard; protein; 192 AA.

XX AAR69640;

DT 25-MAR-2003 (revised)

DT 14-SEP-1995 (first entry)

DE Hepatitis C virus envelope 1 protein isolate SW1.

KM Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate SW1;

XX diagnosis; vaccines; antibodies; antisera; gene inhibition.

OS Hepatitis C virus.

XX WO9501442-A2.

XX 12-JAN-1995.

PF 28-JUN-1994; 94WO-US007320.

PR 29-JUN-1993; 93US-00086428.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Bukh J, Miller RH, Purcell RH;

DR WPI; 1995-061006/08.

DR N-PSDB; AAQ83851.

PT Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
 PT nucleotide(s), peptide(s) and proteins, used in diagnosis and in
 PT vaccines.

PS Claim 3; Page 84-85; 186pp; English.

CC AAQ83851 encodes AAR69640 hepatitis C virus (HCV) envelope 1 (E1) protein
 CC isolate SW1, both can be used for the diagnosis of HCV infection, and in
 CC the prodn. of anti-HCV vaccines, antibodies and antisera. The cDNA may
 CC also be used to inhibit the expression of the HCV E1 gene. (Updated on 25
 CC -MAR-2003 to correct PN field.)

CC Sequence 192 AA;

Query Match 98.4%; Score 182; DB 2; Length 192;
 Best Local Similarity 97.1%; Pred. No. 2e-19;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 34
 DB 116 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 149

RESULT 39

ID AAR69634 standard; protein; 192 AA.

XX AAR69634;

DT 25-MAR-2003 (revised)

DT 14-SEP-1995 (first entry)

DE Hepatitis C virus envelope 1 protein isolate DK7.

KM Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate DK7;

XX diagnosis; vaccines; antibodies; antisera; gene inhibition.

OS Hepatitis C virus.

XX WO9501442-A2.

XX 12-JAN-1995.

```

XX 28-JUN-1994; 94WO-US007320.
PF
XX 29-JUN-1993; 93US-00086428.
PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
PI Burk J, Miller RH, Purcell RH;
XX
XX WPI; 1995-061006/08.
DR N-PSDB; AAQ83845.
XX
PT Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
PT nucleotide(s), peptide(s) and proteins, used in diagnosis and in
PT vaccines.
XX
PS Claim 3; Page 80; 186pp; English.
XX
CC AAQ83845 encodes AAR69637 hepatitis C virus (HCV) envelope 1 (E1) protein
CC isolate DK7, both can be used for the diagnosis of HCV infection, and in
CC the prodn. of anti-HCV vaccines, antibodies and antisera. The cDNA may
CC also be used to inhibit the expression of the HCV E1 gene. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 192 AA;

Query Match 98.4%; Score 182; DB 2; Length 192;
Best Local Similarity 97.1%; Pred. No. 2e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 34
Db 116 SIYPGHITGHRMAMDMNMNSPTTALVVAQLLRI 149

RESULT 40
AAR69637
ID AAR69637 standard; protein; 192 AA.
XX
AC AAR69637;
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1995 (first entry)
XX
DE Hepatitis C virus envelope 1 protein isolate DR4.
XX
XX Hepatitis C virus; HCV; non-A non-B; envelope 1 gene; isolate DR4;
KM diagnosis; vaccines; antibodies; antisera; gene inhibition.
XX
OS Hepatitis C virus.
XX
XX WO9501442-A2.
XX
XX 12-JAN-1995.
XX
XX 28-JUN-1994; 94WO-US007320.
PF
XX 29-JUN-1993; 93US-00086428.
PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Burk J, Miller RH, Purcell RH;
XX
XX WPI; 1995-061006/08.
DR N-PSDB; AAQ83848.
XX
PT Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
PT nucleotide(s), peptide(s) and proteins, used in diagnosis and in
PT vaccines.
XX
PS Claim 3; Page 81-82; 186pp; English.
XX
CC AAQ83848 encodes AAR69637 hepatitis C virus (HCV) envelope 1 (E1) protein

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CC isolate DR4, both can be used for the diagnosis of HCV infection, and in
CC the prodn. of anti-HCV vaccines, antibodies and antisera. The cDNA may
CC also be used to inhibit the expression of the HCV E1 gene. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 192 AA;

Query Match 98.4%; Score 182; DB 2; Length 192;
Best Local Similarity 97.1%; Pred. No. 2e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 34
Db 116 SIYPGHITGHRMAMDMNMNSPTTALVVAQLLRI 149

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Search completed: November 10, 2004, 18:14:36
Job time : 158 secs

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OM protein - protein search, using sw model

Run on: November 10, 2004, 18:09:29 ; Search time 38 Seconds

(without alignments)
59.337 Million cell updates/sec

Title: US-10-685-435-15
Perfect score: 185
Sequence: 1 SIYPGHITGHRMAMDMNMSPTTALVVSQILRI 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/aa/Pctus.COMB.pep.*
6: /cgn2_6/ptodata/1/aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	185	100.0	34	4	US-09-645-470-6
2	185	100.0	34	4	US-09-355-040-23
3	185	100.0	139	3	US-08-444-818-173
4	185	100.0	200	3	US-08-612-973-26
5	185	100.0	200	3	US-08-927-597-26
6	185	100.0	210	3	US-08-612-973-28
7	185	100.0	210	3	US-08-927-597-28
8	185	100.0	212	3	US-08-612-973-4
9	185	100.0	212	3	US-08-927-597-4
10	185	100.0	239	3	US-08-612-973-22
11	185	100.0	239	3	US-08-927-597-22
12	185	100.0	263	3	US-08-612-973-6
13	185	100.0	263	3	US-08-927-597-6
14	185	100.0	692	3	US-08-612-973-48
15	185	100.0	692	3	US-08-927-597-48
16	185	100.0	809	3	US-08-612-973-50
17	185	100.0	809	3	US-08-927-597-50
18	184	99.5	192	1	US-08-086-428B-60
19	184	99.5	192	1	US-08-086-428B-65
20	184	99.5	192	1	US-08-086-428B-70
21	184	99.5	192	1	US-08-086-428B-74
22	184	99.5	192	2	US-08-468-570-60
23	184	99.5	192	2	US-08-468-570-65
24	184	99.5	192	2	US-08-468-570-70
25	184	99.5	192	2	US-08-468-570-74
26	184	99.5	192	2	US-08-290-665A-60
27	184	99.5	192	2	US-08-290-665A-65

28	184	99.5	192	2	US-08-290-665A-70	Sequence 70, Appl
29	184	99.5	192	2	US-08-290-665A-74	Sequence 74, Appl
30	184	99.5	192	4	US-08-466-601A-60	Sequence 60, Appl
31	184	99.5	192	4	US-08-466-601A-65	Sequence 65, Appl
32	184	99.5	192	4	US-08-466-601A-70	Sequence 70, Appl
33	184	99.5	192	4	US-08-466-601A-74	Sequence 74, Appl
34	184	99.5	192	5	PCT-US95-10398-60	Sequence 60, Appl
35	184	99.5	192	5	PCT-US95-10398-65	Sequence 65, Appl
36	184	99.5	192	5	PCT-US95-10398-70	Sequence 70, Appl
37	184	99.5	192	5	PCT-US95-10398-74	Sequence 74, Appl
38	184	99.5	450	4	US-08-635-886C-190	Sequence 190, App
39	184	99.5	450	4	US-08-635-886C-195	Sequence 195, App
40	184	99.5	450	4	US-08-974-690C-190	Sequence 190, App
41	184	99.5	450	4	US-08-974-690C-195	Sequence 195, App
42	182	98.4	192	1	US-08-086-428B-52	Sequence 52, Appl
43	182	98.4	192	1	US-08-086-428B-55	Sequence 55, Appl
44	182	98.4	192	1	US-08-086-428B-56	Sequence 56, Appl
45	182	98.4	192	1	US-08-086-428B-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-09-645-470-6
Sequence 6, Application US/09645470
Patent No. 6521403
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: DELPA, ERIK
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: EPITOPES IN VIRAL ENVELOPE PROTEINS AND SPECIFIC
TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST THESE EPITOPES: USE FOR
FILE REFERENCE: 2551-47
CURRENT APPLICATION NUMBER: US/09/645,470
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/EP99/02154
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: EP 98870060.5
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 34
TYPE: PRT
ORGANISM: Hepatitis C virus
US-09-645-470-6

Query Match 100.0%; Score 185; DB 4; Length 34;
Best Local Similarity 100.0%; Pred No. 5.5e-20;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMSPTTALVVSQILRI 34
Db 1 SIYPGHITGHRMAMDMNMSPTTALVVSQILRI 34

RESULT 2
US-09-355-040-23
Sequence 23, Application US/09355040
Patent No. 6635257
GENERAL INFORMATION:
APPLICANT: DEPLA, ERIK
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, ALFONS
TITLE OF INVENTION: PARTICLES OF HCV ENVELOPE PROTEINS: USE FOR VACCINATION
FILE REFERENCE: DEPLA
CURRENT APPLICATION NUMBER: US/09/355,040
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: PCT/EP99/04342
EARLIER FILING DATE: 1999-06-23

EARLIER APPLICATION NUMBER: EP 98870142.1
EARLIER FILING DATE: 1998-06-24
EARLIER APPLICATION NUMBER: EP 99870033.0
EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 23
LENGTH: 34
TYPE: PRT
ORGANISM: Hepatitis C virus
US-09-355-040-23

Query Match 100.0%; Score 185; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 5,5e-20;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34
DB 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34

RESULT 3

US-08-444-818-173
Sequence 173, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Ailsa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110,002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE: Japanese isolate (T. Miyamura)
US-08-444-818-173

Query Match 100.0%; Score 185; DB 3; Length 139;
Best Local Similarity 100.0%; Pred. No.2.8e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34
DB 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34

DB 8 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 41

RESULT 4

US-08-612-973-26
Sequence 26, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
APPLICANT: MARTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-8714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-612-973-26

Query Match 100.0%; Score 185; DB 3; Length 200;
Best Local Similarity 100.0%; Pred. No. 4.2e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34
DB 166 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 199

RESULT 5

US-08-927-597-26
Sequence 26, Application US/08927597
Patent No. 6245503
GENERAL INFORMATION:
APPLICANT: MARTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.

```

;
; ZIP: 22201-4714
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/612,973
; FILING DATE: 11-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-927-597-26
;
Query Match 100.0%; Score 185; DB 3; Length 200;
Best Local Similarity 100.0%; Pred. No. 4.2e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34
Db 166 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 199

RESULT 6
US-08-612-973-28
; Sequence 28, Application US/08612973
; Patent No. 6150134
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: BOSMAN, FONS
; APPLICANT: DE MARTYNOFF, GUY
; APPLICANT: BUYSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P. C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,973
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 28:
; INFORMATION FOR SEQ ID NO: 28:

```

```

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-612-973-28
;
Query Match 100.0%; Score 185; DB 3; Length 210;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34
Db 166 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 199

RESULT 7
US-08-927-597-28
; Sequence 28, Application US/08927597
; Patent No. 6245503
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: BOSMAN, FONS
; APPLICANT: DE MARTYNOFF, GUY
; APPLICANT: BUYSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P. C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/612,973
; FILING DATE: 11-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-927-597-28
;
Query Match 100.0%; Score 185; DB 3; Length 210;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34
Db 166 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 199

RESULT 8
US-08-612-973-4

```

```
; Sequence 4, Application US/08612973
; Patent No. 6150134
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: BOSMAN, FONS
; APPLICANT: DE MARTYNOFF, GUY
; APPLICANT: BUYSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYTE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,973
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-612-973-4

Query Match      100.0%; Score 185; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.5e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      1 STYPGHITGHRAMDMNMWSPPTALVVSQLLRI 34
DB      139 STYPGHITGHRAMDMNMWSPPTALVVSQLLRI 172

RESULT 9
US-08-927-597-4
; Sequence 4, Application US/08927597
; Patent No. 6285503
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: BOSMAN, FONS
; APPLICANT: DE MARTYNOFF, GUY
; APPLICANT: BUYSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYTE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/612,973
; FILING DATE: 11-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-927-597-4

Query Match      100.0%; Score 185; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.5e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      1 STYPGHITGHRAMDMNMWSPPTALVVSQLLRI 34
DB      139 STYPGHITGHRAMDMNMWSPPTALVVSQLLRI 172

RESULT 10
US-08-612-973-22
; Sequence 22, Application US/08612973
; Patent No. 6150134
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: BOSMAN, FONS
; APPLICANT: DE MARTYNOFF, GUY
; APPLICANT: BUYSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYTE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,973
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

US-08-612-973-22

Query Match 100.0%; Score 185; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 5.1e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 34
|||||
DB 166 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 199

RESULT 11
US-08-927-597-22
; Sequence 22, Application US/08927597
; Patent No. 6245503
; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1467-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-927-597-22

Query Match 100.0%; Score 185; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 5.1e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 34
|||||
DB 166 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 199

RESULT 12
US-08-612-973-6
; Sequence 6, Application US/08612973
; Patent No. 6150134
; GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS

APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1467-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-612-973-6

Query Match 100.0%; Score 185; DB 3; Length 263;
Best Local Similarity 100.0%; Pred. No. 5.7e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 34
|||||
DB 190 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 223

RESULT 13
US-08-927-597-6
; Sequence 6, Application US/08927597
; Patent No. 6245503
; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-927-597-6

Query Match 100.0%; Score 185; DB 3; Length 263;
Best Local Similarity 100.0%; Pred. No. 5,7e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRVAMDMNMWSPPTALVVSQILRI 34
DB 190 SIYPGHITGHRVAMDMNMWSPPTALVVSQILRI 223

RESULT 14
US-08-612-973-48
Sequence 48, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 692 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-612-973-48

Query Match 100.0%; Score 185; DB 3; Length 692;
Best Local Similarity 100.0%; Pred. No. 1,7e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRVAMDMNMWSPPTALVVSQILRI 34
DB 190 SIYPGHITGHRVAMDMNMWSPPTALVVSQILRI 223

RESULT 15
US-08-927-597-48
Sequence 48, Application US/08927597
Patent No. 6245503
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 692 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-927-597-48

Query Match 100.0%; Score 185; DB 3; Length 692;
Best Local Similarity 100.0%; Pred. No. 1,7e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRVAMDMNMWSPPTALVVSQILRI 34
DB 190 SIYPGHITGHRVAMDMNMWSPPTALVVSQILRI 223

RESULT 16
US-08-612-973-50
Sequence 50, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON & VANDERHYTE P.C.
;; STREET: 1100 NORTH GLEBE ROAD
;; CITY: ARLINGTON
;; STATE: VIRGINIA
;; COUNTRY: U.S.A.
;; ZIP: 22201-4714
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/612,973
;; FILING DATE: 11-MAR-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BYRNE, THOMAS E.
;; REGISTRATION NUMBER: 32,205
;; REFERENCE/DOCKET NUMBER: 1487-10
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 50:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 809 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-08-612-973-50
;
Query Match 100.0%; Score 185; DB 3; Length 809;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 1 SIYPGHITGHRMAMDMMMNSPTTALVVSQLLRI 34
Db 307 SIYPGHITGHRMAMDMMMNSPTTALVVSQLLRI 340
;
RESULT 17
US-08-927-597-50
;; Sequence 50, Application US/08927597
;; Patent No. 6245503
;; GENERAL INFORMATION:
;; APPLICANT: MAERTENS, GEERT
;; APPLICANT: BOSMAN, FONS
;; APPLICANT: DE MARTYNOFF, GUY
;; APPLICANT: BUYSSE, MARIE-ANGE
;; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
;; TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
;; NUMBER OF SEQUENCES: 111
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON & VANDERHYTE P.C.
;; STREET: 1100 NORTH GLEBE ROAD
;; CITY: ARLINGTON
;; STATE: VIRGINIA
;; COUNTRY: U.S.A.
;; ZIP: 22201-4714
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/927,597
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/612,973
;; FILING DATE: 11-MAR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BYRNE, THOMAS E.

;; REGISTRATION NUMBER: 32,205
;; REFERENCE/DOCKET NUMBER: 1487-10
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 50:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 809 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-08-927-597-50
;
Query Match 100.0%; Score 185; DB 3; Length 809;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 1 SIYPGHITGHRMAMDMMMNSPTTALVVSQLLRI 34
Db 307 SIYPGHITGHRMAMDMMMNSPTTALVVSQLLRI 340
;
RESULT 18
US-08-086-428B-60
;; Sequence 60, Application US/08086428B
;; Patent No. 5514539
;; GENERAL INFORMATION:
;; APPLICANT: BURK, J., MILLER, R.H. AND
;; APPLICANT: PURCELL, R.H.
;; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
;; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
;; TITLE OF INVENTION: OF SI ISOLATES OF HEPATITIS C AND THE USE
;; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
;; NUMBER OF SEQUENCES: 159
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/086,428B
;; FILING DATE: 29-JUN-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: RICHARD W. BORK
;; REGISTRATION NUMBER: 36,459
;; REFERENCE/DOCKET NUMBER: 2026-4070
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;; INFORMATION FOR SEQ ID NO: 60:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 192 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; ORIGINAL SOURCE:
;; ORGANISM: homosapiens
;; INDIVIDUAL ISOLATE: D1
;;
US-08-086-428B-60
;
Query Match 99.5%; Score 184; DB 1; Length 192;
Best Local Similarity 97.1%; Pred. No. 5.6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPGHITGHRAMDMNMMWSPPTALVVSQLLRI 34
|||||
Db 116 STPGHITGHRAMDMNMMWSPPTALVVSQLLRI 149

RESULT 19

US-08-086-428B-65
; Sequence 65, Application US/08086428B
; Patent No. 5514539
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PORCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 159
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,428B
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: HK5
US-08-086-428B-65

Query Match 99.5%; Score 184; DB 1; Length 192;
Best Local Similarity 97.1%; Pred. No. 5,6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 STPGHITGHRAMDMNMMWSPPTALVVSQLLRI 34
|||||
Db 116 STPGHITGHRAMDMNMMWSPPTALVVSQLLRI 149

RESULT 20

US-08-086-428B-70
; Sequence 70, Application US/08086428B
; Patent No. 5514539
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PORCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE

; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 159
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,428B
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: S9
US-08-086-428B-70

Query Match 99.5%; Score 184; DB 1; Length 192;
Best Local Similarity 97.1%; Pred. No. 5,6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 STPGHITGHRAMDMNMMWSPPTALVVSQLLRI 34
|||||
Db 116 STPGHITGHRAMDMNMMWSPPTALVVSQLLRI 149

RESULT 21

US-08-086-428B-74
; Sequence 74, Application US/08086428B
; Patent No. 5514539
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PORCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 159
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/086,428B
FILING DATE: 29-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: T3
US-08-086-428B-74

Query Match 99.5%; Score 184; DB 1; Length 192;
Best Local Similarity 97.1%; Pred. No. 5,6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMWSPPTALVVSQILRI 34
DB 116 SIYPGHVTHGRAMDMNMWSPPTALVVSQILRI 149

RESULT 22
US-08-468-570-60
Sequence 60, Application US/08468570
Patent No. 5871962
GENERAL INFORMATION:
APPLICANT: BURKH, J., MILLER, R.H. AND
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 159
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
FILING DATE: 6-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: D1
US-08-468-570-60

Query Match 99.5%; Score 184; DB 2; Length 192;
Best Local Similarity 97.1%; Pred. No. 5,6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMWSPPTALVVSQILRI 34
DB 116 SIYPGHVTHGRAMDMNMWSPPTALVVSQILRI 149

RESULT 23
US-08-468-570-65
Sequence 65, Application US/08468570
Patent No. 5871962
GENERAL INFORMATION:
APPLICANT: BURKH, J., MILLER, R.H. AND
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 159
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
FILING DATE: 6-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: HKS
US-08-468-570-65

Query Match 99.5%; Score 184; DB 2; Length 192;
Best Local Similarity 97.1%; Pred. No. 5,6e-19;

STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: D1
US-08-290-665A-60

Query Match 99.5%; Score 184; DB 2; Length 192;
Best Local Similarity 97.1%; Pred. No. 5.6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMWSPITALVVSQILRI 34
Db 116 SIYPGHVTHGRMAMDMNMWSPITALVVSQILRI 149

RESULT 27
US-08-290-665A-65
Sequence 65, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BURKH, J., MILLER, R.H. AND
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: HK5
US-08-290-665A-65

Query Match 99.5%; Score 184; DB 2; Length 192;
Best Local Similarity 97.1%; Pred. No. 5.6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMWSPITALVVSQILRI 34
Db 116 SIYPGHVTHGRMAMDMNMWSPITALVVSQILRI 149

RESULT 28
US-08-290-665A-70
Sequence 70, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BURKH, J., MILLER, R.H. AND
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S9
US-08-290-665A-70

Query Match 99.5%; Score 184; DB 2; Length 192;

Best Local Similarity 97.1%; Pred. No. 5.6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMWMSPTTALVVSQILRI 34
Db 116 SIYPGHVHTGHRAMDMNMWMSPTTALVVSQILRI 149

RESULT 29
US-08-290-665A-74
; Sequence 74, Application US/08290665A
; Patent No. 5882852

; GENERAL INFORMATION:
; APPLICANT: BURK, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792

INFORMATION FOR SEQ. ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

ORGANISM: homosapiens
INDIVIDUAL ISOLATE: T3
US-08-290-665A-74

Query Match 99.5%; Score 184; DB 2; Length 192;
Best Local Similarity 97.1%; Pred. No. 5.6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMWMSPTTALVVSQILRI 34
Db 116 SIYPGHVHTGHRAMDMNMWMSPTTALVVSQILRI 149

RESULT 30
US-08-466-601A-60
; Sequence 60, Application US/08466601A
; Patent No. 6572864

; GENERAL INFORMATION:
; APPLICANT: BURK, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED

; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,601A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070052

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792

INFORMATION FOR SEQ. ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: D1
US-08-466-601A-60

Query Match 99.5%; Score 184; DB 4; Length 192;
Best Local Similarity 97.1%; Pred. No. 5.6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMWMSPTTALVVSQILRI 34
Db 116 SIYPGHVHTGHRAMDMNMWMSPTTALVVSQILRI 149

RESULT 31
US-08-466-601A-65
; Sequence 65, Application US/08466601A
; Patent No. 6572864

; GENERAL INFORMATION:
; APPLICANT: BURK, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.

; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,601A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: HK5
; US-08-466-601A-65

Query Match          99.5%; Score 184; DB 4; Length 192;
Best Local Similarity 97.1%; Pred. No. 5,6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQQLRI 34
Db 116 SIYPGHVTHRMAMDMNMWSPPTALVVSQQLRI 149

RESULT 32
US-08-466-601A-70
; Sequence 70, Application US/08466601A
; Patent No. 6572864
; GENERAL INFORMATION:
; APPLICANT: BURKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,601A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29-JUN-1993

```

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: S9
; US-08-466-601A-70

Query Match          99.5%; Score 184; DB 4; Length 192;
Best Local Similarity 97.1%; Pred. No. 5,6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQQLRI 34
Db 116 SIYPGHVTHRMAMDMNMWSPPTALVVSQQLRI 149

RESULT 33
US-08-466-601A-74
; Sequence 74, Application US/08466601A
; Patent No. 6572864
; GENERAL INFORMATION:
; APPLICANT: BURKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,601A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids

```

TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: T3
US-08-466-601A-74

Query Match 99.5%; Score 184; DB 4; Length 192;
Best Local Similarity 97.1%; Pred. No. 5.6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMWMSPTTALVVSQILRI 34
Db 116 SIYPGHVTHGRAMDMNMWMSPTTALVVSQILRI 149

RESULT 34
PCT-US95-10398-60
Sequence 60, Application PC/TUS9510398

GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: D1
PCT-US95-10398-60

Query Match 99.5%; Score 184; DB 5; Length 192;
Best Local Similarity 97.1%; Pred. No. 5.6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMWMSPTTALVVSQILRI 34
Db 116 SIYPGHVTHGRAMDMNMWMSPTTALVVSQILRI 149

RESULT 35
PCT-US95-10398-65

Sequence 65, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: HKS
PCT-US95-10398-65

Query Match 99.5%; Score 184; DB 5; Length 192;
Best Local Similarity 97.1%; Pred. No. 5.6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMWMSPTTALVVSQILRI 34
Db 116 SIYPGHVTHGRAMDMNMWMSPTTALVVSQILRI 149

RESULT 36
PCT-US95-10398-70

Sequence 70, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND

APPLICANT: PORCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S9
PCT-US95-10398-70

Query Match 99.5%; Score 184; DB 5; Length 192;

Best Local Similarity 97.1%; Pred. No. 5.6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 34
DB 116 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 149

RESULT 37
PCT-US95-10398-74
Sequence 74, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BORK, J., MILLER, R.H. AND
APPLICANT: PORCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK

STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: T3
PCT-US95-10398-74

Query Match 99.5%; Score 184; DB 5; Length 192;
Best Local Similarity 97.1%; Pred. No. 5.6e-19;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 34
DB 116 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 149

RESULT 38
US-08-635-886C-190
Sequence 190, Application US/08635886C
Patent No. 655114
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PatentIn version 3.1
SEQ ID NO 190
LENGTH: 450
TYPE: PRT
ORGANISM: hepatitis C virus
US-08-635-886C-190
Query Match 99.5%; Score 184; DB 4; Length 450;
Best Local Similarity 97.1%; Pred. No. 1.5e-18;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 34
Db 307 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 340

Search completed: November 10, 2004, 18:19:21
Job time : 39 secs

RESULT 39
US-08-635-886C-195
; Sequence 195, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 195
; LENGTH: 450
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-195

Query Match 99.5%; Score 184; DB 4; Length 450;
Best Local Similarity 97.1%; Pred. No. 1.5e-18;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 34
Db 307 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 340

RESULT 40
US-08-974-690C-190
; Sequence 190, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 190
; LENGTH: 450
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-190

Query Match 99.5%; Score 184; DB 4; Length 450;
Best Local Similarity 97.1%; Pred. No. 1.5e-18;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 34
Db 307 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 340

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 10, 2004, 18:18:00 ; Search time 140 Seconds

(without alignments)
85,783 Million cell updates/sec

Title: US-10-685-435-15

Perfect score: 185

Sequence: 1 SIYPGHITGHRMAMDMMNSPTTALVVSQILRI 34

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Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 35322586 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	185	100.0	34	14	US-10-318-200-6
2	185	100.0	34	14	US-10-414-219-23
3	185	100.0	34	16	US-10-685-435-15
4	185	100.0	192	14	US-10-128-590-87
5	185	100.0	192	14	US-10-128-587A-87
6	185	100.0	200	9	US-09-973-025-26
7	185	100.0	200	10	US-09-899-303-26
8	185	100.0	200	10	US-09-995-808-26
9	185	100.0	200	10	US-09-995-860-26
10	185	100.0	200	10	US-09-995-791-26
11	185	100.0	200	16	US-10-321-798-26
12	185	100.0	210	9	US-09-973-025-28
13	185	100.0	210	10	US-09-899-303-28

14	185	100.0	210	10	US-09-995-808-28	Sequence 28, Appl
15	185	100.0	210	10	US-09-995-860-28	Sequence 28, Appl
16	185	100.0	210	10	US-09-995-791-28	Sequence 28, Appl
17	185	100.0	210	16	US-10-321-798-28	Sequence 28, Appl
18	185	100.0	212	9	US-09-973-025-4	Sequence 4, Appl
19	185	100.0	212	10	US-09-899-303-4	Sequence 4, Appl
20	185	100.0	212	10	US-09-995-808-4	Sequence 4, Appl
21	185	100.0	212	10	US-09-995-860-4	Sequence 4, Appl
22	185	100.0	212	10	US-09-995-791-4	Sequence 4, Appl
23	185	100.0	212	16	US-10-321-798-4	Sequence 4, Appl
24	185	100.0	239	9	US-09-973-025-22	Sequence 22, Appl
25	185	100.0	239	10	US-09-899-303-22	Sequence 22, Appl
26	185	100.0	239	10	US-09-995-808-22	Sequence 22, Appl
27	185	100.0	239	10	US-09-995-860-22	Sequence 22, Appl
28	185	100.0	239	10	US-09-995-791-22	Sequence 22, Appl
29	185	100.0	239	16	US-10-321-798-22	Sequence 22, Appl
30	185	100.0	263	9	US-09-973-025-6	Sequence 6, Appl
31	185	100.0	263	10	US-09-899-303-6	Sequence 6, Appl
32	185	100.0	263	10	US-09-995-808-6	Sequence 6, Appl
33	185	100.0	263	10	US-09-995-860-6	Sequence 6, Appl
34	185	100.0	263	10	US-09-995-791-6	Sequence 6, Appl
35	185	100.0	263	16	US-10-321-798-6	Sequence 6, Appl
36	185	100.0	692	9	US-09-973-025-48	Sequence 48, Appl
37	185	100.0	692	10	US-09-899-303-48	Sequence 48, Appl
38	185	100.0	692	10	US-09-995-808-48	Sequence 48, Appl
39	185	100.0	692	10	US-09-995-860-48	Sequence 48, Appl
40	185	100.0	692	10	US-09-995-791-48	Sequence 48, Appl
41	185	100.0	692	16	US-10-321-798-48	Sequence 48, Appl
42	185	100.0	809	9	US-09-973-025-50	Sequence 50, Appl
43	185	100.0	809	10	US-09-899-303-50	Sequence 50, Appl
44	185	100.0	809	10	US-09-995-808-50	Sequence 50, Appl
45	185	100.0	809	10	US-09-995-860-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1

US-10-318-200-6
Sequence 6, Application US/10318200
Publication No. US20030125746A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GERT
APPLICANT: BUUSE, MARIE-ANGE
TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST THESE EPITOPIES: USE FOR
FILE REFERENCE: 2551-47
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US/10/318,200
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/EP99/02154
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: EP 96870060.5
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 6
LENGTH: 34
TYPE: PRT
ORGANISM: Hepatitis C virus
US-10-318-200-6

Query Match 100.0%; Score 185; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 3e+19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMAMDMMNSPTTALVVSQILRI 34
DB 1 SIYPGHITGHRMAMDMMNSPTTALVVSQILRI 34

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RESULT 2
US-10-414-219-23
; Sequence 23, Application US/10414219
; Publication No. US20030202987A1
; GENERAL INFORMATION:
; APPLICANT: DEPLA, ERIK
; APPLICANT: MAERTENS, GEERT
; APPLICANT: BOSMAN, ALFONS
; APPLICANT: VAN WIJNENDAELE, FRANS
; TITLE OF INVENTION: PARTICLES OF HCV ENVELOPE PROTEINS: USE FOR VACCINATION
; FILE REFERENCE: Dep1a
; CURRENT APPLICATION NUMBER: US/10/414,219
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/09/355,040
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: PCT/EP99/04342
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EP 98870142.1
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: EP 99870033.0
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-414-219-23

Query Match          100.0%; Score 185; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMMMSPTTALVVSQILRI 34
DB 1 SIYPGHITGHRMAMDMMMMSPTTALVVSQILRI 34

RESULT 3
US-10-685-435-15
; Sequence 15, Application US/10685435
; Publication No. US20040126754A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Multi-mer peptides derived from Hepatitis C Virus
; TITLE OF INVENTION: envelope proteins for diagnostic use and vaccination
; FILE REFERENCE: PCT98.75.HCV30
; CURRENT APPLICATION NUMBER: US/10/685,435
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US/09/566,266B
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 97870179.5
; PRIOR FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patenting Ver. 2.1
; SEQ ID NO 15
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-685-435-15

Query Match          100.0%; Score 185; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMMMSPTTALVVSQILRI 34
DB 1 SIYPGHITGHRMAMDMMMMSPTTALVVSQILRI 34

RESULT 4
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US-10-128-590-87
; Sequence 87, Application US/10128590
; Publication No. US20030108561A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Core-glycosylated HCV envelope proteins
; FILE REFERENCE: 135 PCT
; CURRENT APPLICATION NUMBER: US/10/128,590
; CURRENT FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 87
; LENGTH: 192
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-128-590-87

Query Match          100.0%; Score 185; DB 14; Length 192;
Best Local Similarity 100.0%; Pred. No. 2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMMMSPTTALVVSQILRI 34
DB 116 SIYPGHITGHRMAMDMMMMSPTTALVVSQILRI 149

RESULT 5
US-10-128-587A-87
; Sequence 87, Application US/10128587A
; Publication No. US20030152940A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Constructs and methods for expression of recombinant HCV envelope
; FILE REFERENCE: 134 PCT
; CURRENT APPLICATION NUMBER: US/10/128,587A
; CURRENT FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 87
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hepatitis C virus
US-10-128-587A-87

Query Match          100.0%; Score 185; DB 14; Length 192;
Best Local Similarity 100.0%; Pred. No. 2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMMMSPTTALVVSQILRI 34
DB 116 SIYPGHITGHRMAMDMMMMSPTTALVVSQILRI 149

RESULT 6
US-09-973-025-26
; Sequence 26, Application US/09973025
; Publication No. US20020182706A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: BOSMAN, FONS
; APPLICANT: DE MARTYNOFF, GUY
; APPLICANT: BUYSSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSER: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
```

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;
; COUNTRY: U.S.A.
; ZIP: 22201-4714
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/973,025
; FILING DATE: 10-Oct-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/612,973
; FILING DATE: 11-MAR-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
;
; INFORMATION FOR SEQ ID NO: 26:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
;
; US-09-973-025-26
;
Query Match          100.0%; Score 185; DB 9; Length 200;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMWSPPTALVVSQILRI 34
DB 166 SIYPGHITGHRAMDMNMWSPPTALVVSQILRI 199

RESULT 7
US-09-899-303-26
; Sequence 26, Application US/09899303
; Publication No. US20030036110a1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; BOSMAN, FONS
; DE MARTINOOF, GUY
; BUYSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,303
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/612,973
; FILING DATE: 11-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
```

```

;
; REFERENCE/DOCKET NUMBER: 1487-10
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
;
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
;
; US-09-899-303-26
;
Query Match          100.0%; Score 185; DB 10; Length 200;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMWSPPTALVVSQILRI 34
DB 166 SIYPGHITGHRAMDMNMWSPPTALVVSQILRI 199

RESULT 8
US-09-995-808-26
; Sequence 26, Application US/09995808
; Publication No. US20030095980A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-70
; CURRENT APPLICATION NUMBER: US/09/995,808
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin 3.1
; SEQ ID NO 26
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Hepatitis C virus
;
; US-09-995-808-26
;
Query Match          100.0%; Score 185; DB 10; Length 200;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMWSPPTALVVSQILRI 34
DB 166 SIYPGHITGHRAMDMNMWSPPTALVVSQILRI 199

RESULT 9
US-09-995-860-26
; Sequence 26, Application US/09995860
; Publication No. US20030118603A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-69
; CURRENT APPLICATION NUMBER: US/09/995,860
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin 3.1
; SEQ ID NO 26
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Hepatitis C virus
;
; US-09-995-860-26
;
Query Match          100.0%; Score 185; DB 10; Length 200;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 SIYPGHITGHRAMDMNMMSPTTALVVSQILRI 34
Db 166 SIYPGHITGHRAMDMNMMSPTTALVVSQILRI 199

RESULT 10
US-09-995-791-26
; Sequence 26, Application US/09995791
; Publication No. US20030147918A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-68
; CURRENT APPLICATION NUMBER: US/09/995,791
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn 3.1
; SEQ ID NO: 26
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-995-791-26

Query Match 100.0%; Score 185; DB 10; Length 200;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRAMDMNMMSPTTALVVSQILRI 34
Db 166 SIYPGHITGHRAMDMNMMSPTTALVVSQILRI 199

RESULT 11
US-10-321-798-26
; Sequence 26, Application US/10321798
; Publication No. US20040126395A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-93
; CURRENT APPLICATION NUMBER: US/10/321,798
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/418,358
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 10/020,510
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn 3.1
; SEQ ID NO: 26
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-321-798-26

Query Match 100.0%; Score 185; DB 16; Length 200;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRAMDMNMMSPTTALVVSQILRI 34
Db 166 SIYPGHITGHRAMDMNMMSPTTALVVSQILRI 199

RESULT 12
US-09-973-025-28
; Sequence 28, Application US/09973025
; Publication No. US20020182706A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; BOSMAN, FONS
; DE MARTYNOFF, GUY

BUYSSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/973,025
FILING DATE: 10-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-973-025-28

Query Match 100.0%; Score 185; DB 9; Length 210;
Best Local Similarity 100.0%; Pred. No. 2,2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRAMDMNMMSPTTALVVSQILRI 34
Db 166 SIYPGHITGHRAMDMNMMSPTTALVVSQILRI 199

RESULT 13
US-09-899-303-28
; Sequence 28, Application US/09899303
; Publication No. US20030036110A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; BOSMAN, FONS
; DE MARTYNOFF, GUY
; BUYSSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/899,303
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/612,973
; FILING DATE: 11-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-899-303-28

Query Match
Best Local Similarity 100.0%; Score 185; DB 10; Length 210;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
DB 166 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 199

RESULT 14
US-09-995-808-28
; Sequence 28, Application US/09995808
; Publication No. US20030095980A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-70
; CURRENT APPLICATION NUMBER: US/09/995,808
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn 3.1
; SEQ ID NO 28
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-995-808-28

Query Match
Best Local Similarity 100.0%; Score 185; DB 10; Length 210;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
DB 166 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 199

RESULT 15
US-09-995-860-28
; Sequence 28, Application US/09995860
; Publication No. US20030118603A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-69
; CURRENT APPLICATION NUMBER: US/09/995,860
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn 3.1
; SEQ ID NO 28
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; LENGTH: 210
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-995-860-28

Query Match
Best Local Similarity 100.0%; Score 185; DB 10; Length 210;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
DB 166 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 199

RESULT 16
US-09-995-791-28
; Sequence 28, Application US/09995791
; Publication No. US20030147918A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-68
; CURRENT APPLICATION NUMBER: US/09/995,791
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn 3.1
; SEQ ID NO 28
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-995-791-28

Query Match
Best Local Similarity 100.0%; Score 185; DB 10; Length 210;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
DB 166 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 199

RESULT 17
US-10-321-798-28
; Sequence 28, Application US/10321798
; Publication No. US20040126395A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-93
; CURRENT APPLICATION NUMBER: US/10/321,798
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/418,358
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 10/020,510
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn 3.1
; SEQ ID NO 28
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-321-798-28

Query Match
Best Local Similarity 100.0%; Score 185; DB 16; Length 210;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
DB 166 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 199
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RESULT 18
US-09-973-025-4
; Sequence 4, Application US/09973025
; Publication No. US20020182706A1
; GENERAL INFORMATION:
; APPLICANT: MARTENS, GEERT
; BOSMAN, FONS
; DE MARTYNOFF, GUY
; BUYSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 10-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US 08/612,973
; FILING DATE: 11-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-973-025-4
Query Match 100.0%; Score 185; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMAMDMNMWMSPTTALVVSQILRI 34
DB 139 SIYPGHITGHRMAMDMNMWMSPTTALVVSQILRI 172
RESULT 19
US-09-899-303-4
; Sequence 4, Application US/09899303
; Publication No. US20030036110A1
; GENERAL INFORMATION:
; APPLICANT: MARTENS, GEERT
; BOSMAN, FONS
; DE MARTYNOFF, GUY
; BUYSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON

STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,303
FILING DATE: 06-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-899-303-4
Query Match 100.0%; Score 185; DB 10; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMAMDMNMWMSPTTALVVSQILRI 34
DB 139 SIYPGHITGHRMAMDMNMWMSPTTALVVSQILRI 172
RESULT 20
US-09-995-808-4
; Sequence 4, Application US/09995808
; Publication No. US20030095980A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-70
; CURRENT APPLICATION NUMBER: US/09/995,808
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin 3.1
; SEQ ID NO 4
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-995-808-4
Query Match 100.0%; Score 185; DB 10; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMAMDMNMWMSPTTALVVSQILRI 34
DB 139 SIYPGHITGHRMAMDMNMWMSPTTALVVSQILRI 172
RESULT 21
US-09-995-860-4
; Sequence 4, Application US/09995860
; Publication No. US20030118603A1
; GENERAL INFORMATION:


```

; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-69
; CURRENT APPLICATION NUMBER: US/09/995,860
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentln 3.1
; SEQ ID NO 4
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-995-860-4

Query Match          100.0%; Score 185; DB 10; Length 212;
Best Local Similarity 100.0%; Pred. No. 2,2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
DB      139 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 172

RESULT 22
US-09-995-791-4
; Sequence 4, Application US/09995791
; Publication No. US20030147918A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-68
; CURRENT APPLICATION NUMBER: US/09/995,791
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentln 3.1
; SEQ ID NO 4
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-995-791-4

Query Match          100.0%; Score 185; DB 10; Length 212;
Best Local Similarity 100.0%; Pred. No. 2,2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
DB      139 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 172

RESULT 23
US-10-321-798-4
; Sequence 4, Application US/10321798
; Publication No. US20040126395A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-93
; CURRENT APPLICATION NUMBER: US/10/321,798
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/418,358
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 10/020,510
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patentln 3.1
; SEQ ID NO 4
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-10-321-798-4
```

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Query Match          100.0%; Score 185; DB 16; Length 212;
Best Local Similarity 100.0%; Pred. No. 2,2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
DB      139 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 172

RESULT 24
US-09-973-025-22
; Sequence 22, Application US/09973025
; Publication No. US20020182706A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; BOSMAN, FONS
; DE MARTYNOFF, GUY
; BUYSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSER: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLOBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/973,025
; FILING DATE: 10-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/612,973
; FILING DATE: 11-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-973-025-22

Query Match          100.0%; Score 185; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 2,5e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
DB      166 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 199

RESULT 25
US-09-899-303-22
; Sequence 22, Application US/09899303
; Publication No. US20030036110A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; BOSMAN, FONS
```

```

DE MARTYNOFF, GUY
BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/09/899,303
FILING DATE: 06-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-899-303-22

Query Match          100.0%; Score 185; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMNMSPTTALVVSQILRI 34
DB 166 SIYPGHITGHRMAMDMMNMSPTTALVVSQILRI 199

RESULT 26
US-09-995-808-22
; Sequence 22, Application US/09995808
; Publication No. US20030095980A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; TITLE OF INVENTION: therapeutic use.
; FILE REFERENCE: 2551-70
; CURRENT APPLICATION NUMBER: US/09/995,808
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentln 3.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Hepatitis C virus

US-09-995-808-22

Query Match          100.0%; Score 185; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMNMSPTTALVVSQILRI 34
DB 166 SIYPGHITGHRMAMDMMNMSPTTALVVSQILRI 199

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DB 166 SIYPGHITGHRMAMDMMNMSPTTALVVSQILRI 199

RESULT 27
US-09-995-860-22
; Sequence 22, Application US/09995860
; Publication No. US20030118603A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; TITLE OF INVENTION: therapeutic use.
; FILE REFERENCE: 2551-69
; CURRENT APPLICATION NUMBER: US/09/995,860
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentln 3.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Hepatitis C virus

US-09-995-860-22

Query Match          100.0%; Score 185; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMNMSPTTALVVSQILRI 34
DB 166 SIYPGHITGHRMAMDMMNMSPTTALVVSQILRI 199

RESULT 28
US-09-995-791-22
; Sequence 22, Application US/09995791
; Publication No. US20030147918A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; TITLE OF INVENTION: therapeutic use.
; FILE REFERENCE: 2551-68
; CURRENT APPLICATION NUMBER: US/09/995,791
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentln 3.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Hepatitis C virus

US-09-995-791-22

Query Match          100.0%; Score 185; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMNMSPTTALVVSQILRI 34
DB 166 SIYPGHITGHRMAMDMMNMSPTTALVVSQILRI 199

RESULT 29
US-10-321-798-22
; Sequence 22, Application US/10321798
; Publication No. US20040126395A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; TITLE OF INVENTION: therapeutic use.
; FILE REFERENCE: 2551-93
; CURRENT APPLICATION NUMBER: US/10/321,798
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/418,358
; PRIOR FILING DATE: 2002-10-16

```

PRIOR APPLICATION NUMBER: 10/020,510
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PatentIn 3.1
SEQ ID NO 22
LENGTH: 239
TYPE: PROT
ORGANISM: Hepatitis C virus
US-10-321-798-22

Query Match 100.0%; Score 185; DB 16; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMADMMNMSPTTALVVSQLLRI 34
DB 166 SIYPGHITGHRMADMMNMSPTTALVVSQLLRI 199

RESULT 30

US-09-973-025-6
Sequence 6, Application US/09973025
Publication No. US20020182706A1
GENERAL INFORMATION:

APPLICANT: MARTENS, GEERT
BOSMAN, FONS

DE MARTINOFF, GUY
BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHVE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/973,025

FILING DATE: 10-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/612,973

FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1487-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-973-025-6
Query Match 100.0%; Score 185; DB 9; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMADMMNMSPTTALVVSQLLRI 34
DB 190 SIYPGHITGHRMADMMNMSPTTALVVSQLLRI 223

RESULT 31
US-09-899-303-6
Sequence 6, Application US/09899303
Publication No. US20030036110A1
GENERAL INFORMATION:

APPLICANT: MARTENS, GEERT
BOSMAN, FONS

DE MARTINOFF, GUY
BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHVE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/899,303

FILING DATE: 06-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/612,973

FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1487-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-899-303-6
Query Match 100.0%; Score 185; DB 10; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIYPGHITGHRMADMMNMSPTTALVVSQLLRI 34
DB 190 SIYPGHITGHRMADMMNMSPTTALVVSQLLRI 223

RESULT 32
US-09-995-808-6
Sequence 6, Application US/0995808
Publication No. US20030095980A1
GENERAL INFORMATION:

APPLICANT: Immunogenetics N.V.
TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
therapeutic use.
FILE REFERENCE: 2551-70
CURRENT APPLICATION NUMBER: US/09/995,808
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn 3.1
SEQ ID NO 6
LENGTH: 263

TYPE: PRT
ORGANISM: Hepatitis C virus
US-09-995-860-6

Query Match 100.0%; Score 185; DB 10; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMNWSPTTALVVSQLLRI 34
190 SIYPGHITGHRMAMDMMNWSPTTALVVSQLLRI 223

RESULT 33
US-09-995-860-6
Sequence 6, Application US/09995860
Publication No. US20030118603A1
GENERAL INFORMATION:

APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
FILE REFERENCE: 2551-69
CURRENT APPLICATION NUMBER: US/09/995,860
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn 3.1
SEQ ID NO 6
LENGTH: 263
TYPE: PRT
ORGANISM: Hepatitis C virus
US-09-995-860-6

Query Match 100.0%; Score 185; DB 10; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMNWSPTTALVVSQLLRI 34
190 SIYPGHITGHRMAMDMMNWSPTTALVVSQLLRI 223

RESULT 34
US-09-995-791-6
Sequence 6, Application US/09995791
Publication No. US20030147918A1
GENERAL INFORMATION:

APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
FILE REFERENCE: 2551-68
CURRENT APPLICATION NUMBER: US/09/995,791
CURRENT FILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn 3.1
SEQ ID NO 6
LENGTH: 263
TYPE: PRT
ORGANISM: Hepatitis C virus
US-09-995-791-6

Query Match 100.0%; Score 185; DB 10; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMNWSPTTALVVSQLLRI 34
190 SIYPGHITGHRMAMDMMNWSPTTALVVSQLLRI 223

RESULT 35
US-10-321-798-6
Sequence 6, Application US/10321798
Publication No. US20040126395A1

GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
FILE REFERENCE: 2551-93
CURRENT APPLICATION NUMBER: US/10/321,798
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: 60/418,358
PRIOR FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 10/020,510
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PatentIn 3.1
SEQ ID NO 6
LENGTH: 263
TYPE: PRT
ORGANISM: Hepatitis C virus
US-10-321-798-6

Query Match 100.0%; Score 185; DB 16; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.8e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMNWSPTTALVVSQLLRI 34
Db 190 SIYPGHITGHRMAMDMMNWSPTTALVVSQLLRI 223

RESULT 36
US-09-973-025-48
Sequence 48, Application US/09973025
Publication No. US20020182706A1
GENERAL INFORMATION:

APPLICANT: MAERTENS, GERT
BOGMAN, FONS
DE MARTYNOFF, GUY
BOYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/973,025
FILING DATE: 10-Oct-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 692 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:

US-09-973-025-48

Query Match 100.0%; Score 185; DB 9; Length 692;
Best Local Similarity 100.0%; Pred. No. 8.1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
DB 190 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 223

RESULT 37

US-09-899-303-48
; Sequence 48, Application US/09899303
; Publication No. US20030036110A1
; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT

BOSMAN, FONS

DE MARTYNOFF, GUY

BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE

PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/899,303

FILING DATE: 06-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/612,973

FILING DATE: 11-Mar-1996

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1487-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 692 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 48:

US-09-899-303-48

Query Match 100.0%; Score 185; DB 10; Length 692;
Best Local Similarity 100.0%; Pred. No. 8.1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 38

US-09-995-808-48
; Sequence 48, Application US/09995808
; Publication No. US20030095980A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.

; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; FILE REFERENCE: 2551-70
; CURRENT APPLICATION NUMBER: US/09/995,808
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin 3.1
; SEQ ID NO 48
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-995-808-48

US-09-995-808-48

Query Match 100.0%; Score 185; DB 10; Length 692;
Best Local Similarity 100.0%; Pred. No. 8.1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
DB 190 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 223

RESULT 39

US-09-995-860-48
; Sequence 48, Application US/09995860
; Publication No. US20030118603A1
; GENERAL INFORMATION:

APPLICANT: Innogenetics N.V.

TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and

FILE REFERENCE: 2551-69

CURRENT APPLICATION NUMBER: US/09/995,860

CURRENT FILING DATE: 2001-11-29

NUMBER OF SEQ ID NOS: 122

SOFTWARE: Patentin 3.1

SEQ ID NO 48

LENGTH: 692

TYPE: PRT

ORGANISM: Hepatitis C virus

US-09-995-860-48

Query Match 100.0%; Score 185; DB 10; Length 692;
Best Local Similarity 100.0%; Pred. No. 8.1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
DB 190 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 223

RESULT 40

US-09-995-791-48
; Sequence 48, Application US/09995791
; Publication No. US20030147918A1
; GENERAL INFORMATION:

APPLICANT: Innogenetics N.V.

TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and

FILE REFERENCE: 2551-68

CURRENT APPLICATION NUMBER: US/09/995,791

CURRENT FILING DATE: 2001-11-29

NUMBER OF SEQ ID NOS: 122

SOFTWARE: Patentin 3.1

SEQ ID NO 48

LENGTH: 692

TYPE: PRT

ORGANISM: Hepatitis C virus

US-09-995-791-48

Query Match 100.0%; Score 185; DB 10; Length 692;
Best Local Similarity 100.0%; Pred. No. 8.1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMAMMSPTTALVVSQILRI 34
Db 190 SIYPGHITGHRMAMDMAMMSPTTALVVSQILRI 223

Search completed: November 10, 2004, 18:30:03
Job time : 141 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2004, 18:09:09 / Search time 37 Seconds

(without alignments)
88.415 Million cell updates/sec

Title: US-10-685-435-15

Perfect score: 185
Sequence: 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 79: *
1: p1:1: *
2: p1:2: *
3: p1:3: *
4: p1:4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184	99.5	177	2 S25123	genome polyprotein
2	184	99.5	177	2 S32743	genome polyprotein
3	184	99.5	550	2 JH0711	genome polyprotein
4	184	99.5	3010	1 GNMVTV	genome polyprotein
5	183	98.9	177	2 S32745	genome polyprotein
6	182	98.4	177	2 S32749	genome polyprotein
7	181	97.8	177	2 S32746	genome polyprotein
8	181	97.8	640	2 UQ1584	genome polyprotein
9	180	97.3	177	2 S32741	genome polyprotein
10	180	97.3	315	2 PNO011	genome polyprotein
11	180	97.3	787	2 PNO677	genome polyprotein
12	180	97.3	3010	1 A45573	hypothetical prote
13	180	97.3	3010	1 GNMVCT	genome polyprotein
14	180	97.3	3010	1 GNMVTC	genome polyprotein
15	179	96.8	322	2 UN0265	genome polyprotein
16	179	96.8	513	2 PC1284	genome polyprotein
17	179	96.8	3011	1 GNMVWC	genome polyprotein
18	178	96.2	315	2 PS0164	genome polyprotein
19	178	96.2	782	2 S18032	envelope glycoprot
20	178	96.2	3010	1 S18030	genome polyprotein
21	178	95.7	513	2 A44150	genome polyprotein
22	176	95.1	369	2 S21471	structural protein
23	175	94.6	520	2 S12707	genome polyprotein
24	175	94.6	441	2 JQ1925	genome polyprotein
25	174	94.1	782	2 S19875	genome polyprotein
26	174	94.1	3011	1 S40770	genome polyprotein
27	173	93.5	315	2 PS0165	envelope glycoprot
28	173	93.5	415	2 PC4407	envelope protein -
29	173	93.5	523	2 JQ1926	polyprotein - hepa

30	172	93.0	782	2 S19876	genome polyprotein
31	172	93.0	3011	1 GNMVCH	genome polyprotein
32	170	91.9	782	2 S18031	genome polyprotein
33	162	87.6	3014	1 JCS620	genome polyprotein
34	151	81.6	492	2 S41288	genome polyprotein
35	148	80.0	411	2 PC2060	genome polyprotein
36	148	80.0	411	2 PC2061	genome polyprotein
37	147	79.5	193	2 S35630	genome polyprotein
38	143	77.3	874	2 JQ0881	genome polyprotein
39	143	77.3	3033	1 JQ1303	genome polyprotein
40	138	74.6	874	2 JQ0883	genome polyprotein
41	133	71.9	3033	1 GNMV08	genome polyprotein
42	110	59.5	284	2 PS0104	genome polyprotein
43	75	40.5	259	2 PS0102	genome polyprotein
44	65	35.1	180	2 PC1305	genome polyprotein
45	65	35.1	180	2 PC1304	genome polyprotein

ALIGNMENTS

RESULT 1
S25123
genome polyprotein (clone Glob 1) - hepatitis C virus (fragment)
N/Contains: envelope protein E1
C/Species: hepatitis C virus
C/Date: 20-Feb-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: S25123
R/Hoehne, M.; Schreier, E.; Fuchs, K.; Wiese, M.; Deinhardt, F.; Roggendorf, M.
submitted to the EMBL Data Library, April 1992
A/Description: Variability of E1 gene region of Hepatitis C virus in patients infected
A/Reference number: S25123
A/Accession: S25123
A/Molecule type: genomic RNA
A/Residues: 1-177 <HOB>
A/Cross-references: UNIPROT:Q68909; EMBL:X67299; NID:G59470; PIDN:CAA47713.1; PID:G59471
C/Superfamily: hepatitis C virus genome polyprotein
C/Keywords: envelope protein; polyprotein
F1-177/Product: envelope protein E1 #status predicted <MAT>

Query Match 99.5%; Score 184; DB 2; Length 177;
Best Local Similarity 97.1%; Pred. No. 1.4e-18;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
Db 111 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 144

RESULT 2

S32743
genome polyprotein - hepatitis C virus (isolate EG-1) (fragment)
N/Contains: envelope protein E1
C/Species: hepatitis C virus
A/Variety: isolate EG-1
C/Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
R/Roggendorf, M.; Lu, M.; Fuchs, G.; Ernst, G.; Hoehne, M.; Schreier, E.
submitted to the EMBL Data Library, February 1993
A/Description: Variability of the envelope regions of HCV in European isolates and its s
A/Reference number: S32741
A/Accession: S32743
A/Molecule type: genomic RNA
A/Residues: 1-177 <ROG>
A/Cross-references: UNIPROT:Q06618; EMBL:X72980; NID:G296104; PIDN:CAA51465.1; PID:G2961
A/Experimental source: isolate EG-1
C/Superfamily: hepatitis C virus genome polyprotein
C/Keywords: envelope protein; polyprotein
F1-177/Product: envelope protein E1 #status predicted <MAT>

Query Match 99.5%; Score 184; DB 2; Length 177;
Best Local Similarity 97.1%; Pred. No. 1.4e-18;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 34
 DB 111 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 144

RESULT 3
 JH0711
 genome polypeptide - hepatitis C virus (strain PRCl) (fragments)
 N:Contains: envelope protein E1; envelope protein E2; nonstructural protein NS1; nonstru
 C:Species: hepatitis C virus
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #ext_change 09-Jul-2004
 C:Accession: JH0711
 R:Lin, K.; Hu, Z.; Li, H.; Prince, A.M.; Inchausti, G.
 Gene 144, 245-250, 1992
 A:Title: Genomic typing of hepatitis C viruses present in China.
 A:Reference number: JH0711; PMID:92290283; PMID:1318245
 A:Accession: JH0711
 A:Molecule type: genomic RNA
 A:Residues: 1-550 <Liu>
 A:Cross-references: UNIPROT:Q7LZY4; GB:M74888; GB:M74889
 A>Note: the nucleotide sequence is not complete
 A>Note: translation of the nucleotide sequence is not complete
 C:Superfamily: hepatitis C virus genome polypeptide
 C:Keywords: envelope protein; glycoprotein; nonstructural protein; nucleocapsid; polypro
 F:1-190/Product: envelope protein E1 #status predicted <CPC>
 F:191-380/Product: nucleocapsid protein C #status predicted <CPC>
 F:381-514/Product: envelope protein E2 or nonstructural protein NS1 (fragment) #status p
 F:515-550/Product: nonstructural protein NS5 (fragment) #status predicted <NS5>
 F:196,233,250,305,416,422,429,447/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 99.5%; Score 184; DB 2; Length 550;
 Best Local Similarity 97.1%; Pred. No. 5,1e-18;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 34
 DB 307 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 340

RESULT 4
 GNMWTM
 genome polypeptide - hepatitis C virus (strain Taiwan)
 N:Contains: capsid protein C; envelope protein M; hepatitisin (EC 3.4.21.98) (nonstructu
 protein NS4b; nonstructural protein NS4b; nonstructural protein NS5
 C:Species: hepatitis C virus
 A>Note: host Homo sapiens (man)
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #ext_change 09-Jul-2004
 C:Accession: A40244
 R:Chen, P.U.; Lin, M.H.; Tai, K.F.; Lin, P.C.; Lin, C.U.; Chen, D.S.
 Virology 188, 102-113, 1992
 A:Title: The Taiwanese hepatitis C virus genome: sequence determination and mapping the
 A:Reference number: A40244; PMID:9230206; PMID:1314449
 A:Accession: A40244
 A:Molecule type: genomic RNA
 A:Residues: 1-3010 <Chen>
 A:Cross-references: UNIPROT:P29846; GB:M84754
 C:Superfamily: hepatitis C virus genome polypeptide
 C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
 F:1-115/Product: capsid protein C #status predicted <CPC>
 F:116-191/Product: envelope protein M #status predicted <EMP>
 F:192-389/Product: major envelope protein B #status predicted <MB>
 F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
 F:1007-1615/Product: hepatitisin #status predicted <NS3>
 F:1230-1237/Region: nucleotide-binding motif A (P-loop)
 F:1312-1317/Region: nucleotide-binding motif B
 F:1316-1319/Region: DEXH motif
 F:1616-1662/Product: nonstructural protein NS4b #status predicted <NS4b>
 F:1663-2013/Product: nonstructural protein NS5 #status predicted <NS5>
 F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
 F:196,209,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,207

Query Match 99.5%; Score 184; DB 1; Length 3010;
 Best Local Similarity 97.1%; Pred. No. 3.4e-17;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 34
 DB 307 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 340

RESULT 5
 S32745
 genome polypeptide - hepatitis C virus (isolate EG-2) (fragment)
 N:Contains: envelope protein E1
 C:Species: hepatitis C virus
 A:Variety: isolate EG-2
 C>Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #ext_change 09-Jul-2004
 C:Accession: S32745
 R:Rogendorf, M.; Lu, M.; Fuchs, G.; Ernst, G.; Hoehne, M.; Schreier, E.
 submitted to the EMBL Data Library, February 1993
 A:Description: Variability of the envelope regions of HCV in European isolates and its s
 A:Reference number: S32741
 A:Accession: S32745
 A:Molecule type: genomic RNA
 A:Residues: 1-177 <ROG>
 A:Cross-references: UNIPROT:Q06619; EMBL:X72982; NID:G296108; PID:CAA51487.1; PID:G2961
 A:Experimental source: isolate EG-2
 C:Superfamily: hepatitis C virus genome polypeptide
 C:Keywords: envelope protein; polypeptide
 F:1-177/Product: envelope protein E1 #status predicted <MAT>

Query Match 98.3%; Score 183; DB 2; Length 177;
 Best Local Similarity 97.1%; Pred. No. 2e-18;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 34
 DB 111 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 144

RESULT 6
 S32749
 genome polypeptide - hepatitis C virus (isolate RU-1) (fragment)
 N:Contains: envelope protein E1
 C:Species: hepatitis C virus
 A:Variety: isolate RU-1
 C>Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #ext_change 09-Jul-2004
 C:Accession: S32749
 R:Rogendorf, M.; Lu, M.; Fuchs, G.; Ernst, G.; Hoehne, M.; Schreier, E.
 submitted to the EMBL Data Library, February 1993
 A:Description: Variability of the envelope regions of HCV in European isolates and its s
 A:Reference number: S32741
 A:Accession: S32749
 A:Molecule type: genomic RNA
 A:Residues: 1-177 <ROG>
 A:Cross-references: UNIPROT:Q06613; EMBL:X72975; NID:G296114; PID:CAA51480.1; PID:G2961
 A:Experimental source: isolate RU-1
 C:Superfamily: hepatitis C virus genome polypeptide
 C:Keywords: envelope protein; polypeptide
 F:1-177/Product: envelope protein E1 #status predicted <MAT>

Query Match 98.4%; Score 182; DB 2; Length 177;
 Best Local Similarity 94.1%; Pred. No. 2.8e-18;
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Query 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 34
 DB 111 SIYPGHITGHRMAMDMNMNSPTTALVVSQQLRI 144

RESULT 7
 S32746
 genome polypeptide - hepatitis C virus (isolate HU-1) (fragment)
 N:Contains: envelope protein E1

C:Species: hepatitis C virus
A:Variety: isolate HU-1
C:Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S32746
R:Roggendorf, M.; Lu, M.; Fuchs, G.; Ernst, G.; Hoehne, M.; Schreier, E.
Submitted to the EMBL Data Library, February 1993
A:Description: Variability of the envelope regions of HCV in European isolates and its s
A:Reference number: S32741
A:Accession: S32746
A:Molecule type: genomic RNA
A:Residues: 1-177 <ROG>
A:Cross-references: UNIPROT:Q06612; EMBL:X72976; NID:G296110; PIDN:CAAS1483.1; PID:G2961
A:Experimental source: isolate HU-1
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: envelope protein; polypeptide
F:1-177/Product: envelope protein E1 #status predicted <MAT>

Query Match 97.8%; Score 181; DB 2; Length 177;
Best Local Similarity 97.1%; Pred. No. 3.8e-18;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SIYPGHTGHRAMDMNMWSPPTALVVSQQLRI 34
DB 111 SIYPGHISGHRAMDMNMWSPPTALVVSQQLRI 144

RESULT 8
QJ1584
genome polypeptide - hepatitis C virus (strain U.K.) (fragment)
N:Contains: core protein C; envelope protein E1; envelope protein E2; nonstructural prot
C:Species: hepatitis C virus
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: QJ1584
J:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992
A:Title: Cloning and sequencing of the structural region and expression of putative core
A:Reference number: QJ1584; MUID:92300349; PMID:1318944
A:Accession: QJ1584
A:Molecule type: genomic RNA
A:Residues: 1-640 <KUM>
A:Cross-references: UNIPROT:Q68966; GB:X84079; NID:G643119; PIDN:CAAS8888.1; PID:G643120
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: core protein; envelope protein; glycoprotein; nonstructural protein; polypep
F:1-191/Product: core protein C #status predicted <CPC>
F:192-389/Product: envelope protein E1 #status predicted <EE1>
F:390-640/Product: envelope protein E2 and nonstructural protein NS1 #status predicted <
F:196,209,234,305,417,430,448,476,540,556,576,623/Binding site: carbohydrate (Asn) (cov

Query Match 97.8%; Score 181; DB 2; Length 640;
Best Local Similarity 94.1%; Pred. No. 1.6e-17;
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SIYPGHTGHRAMDMNMWSPPTALVVSQQLRI 34
DB 307 SIYPGHISGHRAMDMNMWSPPTALVVSQQLRI 340

RESULT 9
S32741
genome polypeptide - hepatitis C virus (isolate CR-1) (fragment)
N:Contains: envelope protein E1
C:Species: hepatitis C virus
A:Variety: isolate CR-1
C:Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S32741
R:Roggendorf, M.; Lu, M.; Fuchs, G.; Ernst, G.; Hoehne, M.; Schreier, E.
Submitted to the EMBL Data Library, February 1993
A:Description: Variability of the envelope regions of HCV in European isolates and its s
A:Reference number: S32741
A:Accession: S32741
A:Molecule type: genomic RNA
A:Residues: 1-177 <ROG>
A:Cross-references: UNIPROT:Q06617; EMBL:X72978; NID:G296100; PIDN:CAAS1483.1; PID:G2961

A:Experimental source: isolate CR-1
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: envelope protein; polypeptide
F:1-177/Product: envelope protein E1 #status predicted <MAT>

Query Match 97.3%; Score 180; DB 2; Length 177;
Best Local Similarity 94.1%; Pred. No. 5.3e-18;
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SIYPGHTGHRAMDMNMWSPPTALVVSQQLRI 34
DB 111 SIYPGHISGHRAMDMNMWSPPTALVVSQQLRI 144

RESULT 10
PN0011
envelope glycoprotein (clone 63) - hepatitis C virus (fragment)
C:Species: hepatitis C virus
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
C:Accession: PN0011
R:Hijikata, M.; Kato, N.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Shimotohno, K.
Biochem. Biophys. Res. Commun. 175, 220-228, 1991
A:Title: Hypervariable regions in the putative glycoprotein of hepatitis C virus.
A:Reference number: PN0011; MUID:9151353; PMID:1847805
A:Accession: PN0011
A:Molecule type: genomic RNA
A:Residues: 1-315 <HIJ>
A:Cross-references: UNIPROT:Q00904; GB:D00689
A:Note: the authors translated the codon GAC for residue 27 as Glu and GAT for residue 1:
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: glycoprotein; polypeptide
F:200-209/Region: hypervariable 1 #status predicted
F:283-289/Region: hypervariable 2 #status predicted
F:5,18,43,59,114,134,226,232,239,257/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 97.3%; Score 180; DB 2; Length 315;
Best Local Similarity 94.1%; Pred. No. 1e-17;
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SIYPGHTGHRAMDMNMWSPPTALVVSQQLRI 34
DB 116 SIYPGHISGHRAMDMNMWSPPTALVVSQQLRI 149

RESULT 11
PN0677
hypothetical protein 787 - hepatitis C virus (fragment)
C:Species: hepatitis C virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: PN0677
R:Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
Biochem. Biophys. Res. Commun. 196, 780-788, 1993
A:Title: Genetic typing of hepatitis C viruses from Korean patients: Implications of gen
A:Reference number: PN0677; MUID:94059104; PMID:8240354
A:Accession: PN0677
A:Molecule type: mRNA
A:Residues: 1-787 <CHO>
A:Cross-references: UNIPROT:Q08244; GB:I20498; NID:G1381031; PIDN:AAB02608.1; PID:G13810
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: glycoprotein; nonstructural protein
F:196,209,234,250,305,325,421,427,452,536,544,560,580,627,649/Binding site: carbohydrate

Query Match 97.3%; Score 180; DB 2; Length 787;
Best Local Similarity 94.1%; Pred. No. 2.8e-17;
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SIYPGHTGHRAMDMNMWSPPTALVVSQQLRI 34
DB 307 SIYPGHISGHRAMDMNMWSPPTALVVSQQLRI 340

RESULT 12
A45573

genome polyprotein - hepatitis C virus (strain JT)
 N:Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
 protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C:Species: hepatitis C virus
 C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
 R:Tanaka, T.; Kato, N.; Nakagawa, M.; Ootsuyama, Y.; Cho, M.T.; Nakazawa, T.; Hijikata,
 Y. Res. 23, 39-53, 1992
 A:Title: Molecular cloning of hepatitis C virus genome from a single Japanese carrier: S
 A:Reference number: A45573; MUID:92295714; PMID:1318627
 A:Accession: A45573
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-3010 <TAN>
 A:Cross-references: UNIPROT:Q00269; GB:D11168; GB:D01171; NID:g221612; PIDN:BA01943.1;
 A:Experimental source: RCY-JT
 A>Note: sequence extracted from NCBI backbone (NCBIN:106206, NCBI:P:106207)
 C:Superfamily: hepatitis C virus genome polyprotein
 C:Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin
 F:2-115/Product: capsid protein C #status predicted <CPC>
 F:116-191/Product: envelope protein M #status predicted <EPM>
 F:192-389/Product: major envelope protein E #status predicted <MEB>
 F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
 F:1007-1615/Product: hepacivirin #status predicted <NS3>
 F:1230-1237/Region: nucleotide-binding motif A (P-loop)
 F:1312-1317/Region: nucleotide-binding motif B
 F:1316-1319/Region: DEXH motif
 F:1616-1862/Product: nonstructural protein NS4a #status predicted <NS4a>
 F:1863-2013/Product: nonstructural protein NS4b #status predicted <NS4b>
 F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>

Query Match 97.3%; Score 180; DB 1; Length 3010;
 Best Local Similarity 94.1%; Pred. No. 1.3e-16;
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 34
 DB 307 SIYPGHVSGHRMAMDMNMWSPPTALVVSQILRI 340

RESULT 13
 GNMVTC
 genome polyprotein - hepatitis C virus (strain J)
 N:Contains: capsid protein C; envelope protein M; major envelope protein E; nonstructura
 protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C:Species: hepatitis C virus
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: A39253; PS0086
 R:Kato, N.; Hijikata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimoch
 Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990
 A:Title: Molecular cloning of the human hepatitis C virus genome from Japanese patients
 A:Reference number: A39253; MUID:91088550; PMID:2175903
 A:Accession: A39253
 A:Molecule type: genomic RNA
 A:Residues: 1-3010 <KAT>
 A:Cross-references: UNIPROT:P26662; GB:D90208; NID:g221610; PIDN:BA01423.1; PID:g221611
 R:Kato, N.; Ohkoshi, S.; Shimotohno, K.
 Proc. Jpn. Acad. 65B, 219-223, 1989
 A:Title: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence vari
 A:Reference number: PS0085
 A:Accession: PS0085
 A:Molecule type: genomic RNA
 A:Residues: 2650-2707 <KAT>
 A:Experimental source: Japanese isolate
 C:Comment: The cleavage sites of this polyprotein have not been determined.
 C:Superfamily: hepatitis C virus genome polyprotein
 C:Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin
 F:2-115/Product: capsid protein C #status predicted <CPC>
 F:116-191/Product: envelope protein M #status predicted <EPM>
 F:192-389/Product: major envelope protein E #status predicted <MEB>
 F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>

F:1007-1615/Product: hepacivirin #status predicted <NS3>
 F:1230-1237/Region: nucleotide-binding motif A (P-loop)
 F:1312-1317/Region: nucleotide-binding motif B
 F:1316-1319/Region: DEXH motif
 F:1616-1862/Product: nonstructural protein NS4a #status predicted <NS4a>
 F:1863-2013/Product: nonstructural protein NS4b #status predicted <NS4b>
 F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
 F:196,209,234,250,305,325,417,423,430,448,532,556,576,623,645,1213,1255,2041,2077,2240,2

Query Match 97.3%; Score 180; DB 1; Length 3010;
 Best Local Similarity 94.1%; Pred. No. 1.3e-16;
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 34
 DB 307 SIYPGHVSGHRMAMDMNMWSPPTALVVSQILRI 340

RESULT 14
 GNMVTC
 genome polyprotein - hepatitis C virus
 N:Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
 protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C:Species: hepatitis C virus
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C:Accession: A38465
 R:Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, E.;
 J. Virol. 65, 1105-1113, 1991
 A:Title: Structure and organization of the hepatitis C virus genome isolated from human
 A:Reference number: A38465; MUID:91140698; PMID:1847440
 A:Accession: A38465
 A:Molecule type: genomic RNA
 A:Residues: 1-3010 <TAK>
 A:Cross-references: UNIPROT:P26663; EMBL:M58335; NID:g329770; PIDN:AAA72945.1; PID:g3297
 C:Superfamily: hepatitis C virus genome polyprotein
 C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
 F:2-115/Product: capsid protein C #status predicted <CPC>
 F:116-191/Product: envelope protein M #status predicted <EPM>
 F:192-389/Product: major envelope protein E #status predicted <MEB>
 F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
 F:1007-1615/Product: hepacivirin #status predicted <NS3>
 F:1230-1237/Region: nucleotide-binding motif A (P-loop)
 F:1312-1317/Region: nucleotide-binding motif B
 F:1316-1319/Region: DEXH motif
 F:1616-1862/Product: nonstructural protein NS4a #status predicted <NS4a>
 F:1863-2013/Product: nonstructural protein NS4b #status predicted <NS4b>
 F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
 F:196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,2077,22

Query Match 97.3%; Score 180; DB 1; Length 3010;
 Best Local Similarity 94.1%; Pred. No. 1.3e-16;
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGRMAMDMNMWSPPTALVVSQILRI 34
 DB 307 SIYPGHVSGHRMAMDMNMWSPPTALVVSQILRI 340

RESULT 15
 UN0265
 genome polyprotein - hepatitis C virus (isolate GM2) (fragments)
 N:Contains: amino end of envelope protein M; carboxyl end of capsid protein C; fragment
 C:Species: hepatitis C virus
 A>Note: host Homo sapiens (man)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
 C:Accession: UN0265
 R:Riches, K.; Mott, M.; Schreier, E.; Zachoval, R.; Deinhardt, F.; Roggendorf, M.
 Gene 103, 163-169, 1991
 A:Title: Characterization of nucleotide sequences from European hepatitis C virus isolat
 A:Reference number: UN0265; MUID:91365241; PMID:1653756
 A:Accession: UN0265
 A:Molecule type: genomic RNA

A:Residues: 1-322 <FUC>
A:Cross-references: UNIPROT:Q03729; GB:M61717; GB:M61718
A>Note: the authors translated the codon ACG for residue 198 as Tyr
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: capsid protein; envelope protein; glycoprotein; polypeptide; transmembrane F
F11-109/Product: capsid protein C (fragment) #status predicted <COR>
F110-178/Product: envelope protein M (fragment) #status predicted <EPM>
F163-178/Product: transmembrane #status predicted <TM1>
F179-322/Product: major envelope protein E (fragment) #status predicted <ENV>
F1253-269/Product: transmembrane #status predicted <TM2>
F191.216/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 96.8%; Score 179; DB 2; Length 322;
Best Local Similarity 94.1%; Pred. No. 1.4e-17;
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRAMDMMMWSPPTALVVSQQLRI 34
Db 289 SIYPGHITGHRAMDMMMWSPPTALVVAQLVRI 322

RESULT 16
PC1284
genome polypeptide - hepatitis C virus (isolate HC-34) (fragment)
C:Species: hepatitis C virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: PC1284
R:Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsunoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda, Jpn. J. Exp. Med. 60, 167-177, 1990
A>Title: The 5'-terminal sequence of the hepatitis C virus genome.
A:Reference number: PC1284; MUID:91013116; PMID:2170712
A:Accession type: genomic RNA
A:Residues: 1-513 <OK>
A:Cross-references: UNIPROT:Q81221; GB:D00832; NID:G221513; PIDN:BAA00706.1; PID:G221514
C:Superfamily: hepatitis C virus genome polypeptide

Query Match 96.8%; Score 179; DB 2; Length 513;
Best Local Similarity 94.1%; Pred. No. 2.4e-17;
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRAMDMMMWSPPTALVVSQQLRI 34
Db 307 SIYPGHITGHRAMDMMMWSPPTALVVSQQLRI 340

RESULT 17
GNMVG3
genome polypeptide - hepatitis C virus (strain HCV-1)
N:Contains: capsid protein C; envelope protein M; hepadityrin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C/Accession: A39166; PQ0403; PQ0404
R:Choo, Q.L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Gallegos, C.; Coi
Proc. Natl. Acad. Sci. U.S.A. 88, 2451-2455, 1991
A>Title: Genetic organization and diversity of the hepatitis C virus.
A:Reference number: A39166; MUID:91172826; PMID:1846704
A:Accession: A39166
A:Accession type: mRNA
A:Residues: 1-3011 <CHO>
A:Cross-references: UNIPROT:P26664; GB:M62321; NID:G329873; PIDN:AAA45676.1; PID:G329874
R:Chan, S.W.; Moomsh, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.L
J. Gen. Virol. 73, 1131-1141, 1992
A>Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to e
A:Reference number: PQ0393; MUID:92268671; PMID:1316939
A:Accession: PQ0403
A:Accession type: genomic RNA
A:Residues: 1577-1633 <CHA>
A:Cross-references: DDBJ:D10128
A:Experimental source: isolates E-b16
A:Accession: PQ0404
A>Status: preliminary

A:Molecule type: genomic RNA
A:Residues: 1577-1633 <CH2>
A:Experimental source: isolates E-b17
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: ACP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
F11-115/Product: capsid protein C #status predicted <CPC>
F116-191/Product: envelope protein M #status predicted <EPM>
F192-389/Product: major envelope protein E #status predicted <ME>
F139-729/Product: nonstructural protein NS1 #status predicted <NS1>
F1730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F1007-1615/Product: hepacivirin #status predicted <NS3>
F1230-1237/Region: nucleotide-binding motif A (P-loop)
F1312-1317/Region: nucleotide-binding motif B
F1316-1319/Region: DEXH motif
F1616-1862/Product: nonstructural protein NS4a #status predicted <NS4>
F1663-2013/Product: nonstructural protein NS4b #status predicted <NS4b>
F1204-2011/Product: nonstructural protein NS5 #status predicted <NS5>
F1196,209,234,305,325,417,423,430,446,476,532,540,556,576,623,645,1213,1255,2041,2077,22

Query Match 96.8%; Score 179; DB 1; Length 3011;
Best Local Similarity 94.1%; Pred. No. 1.7e-16;
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRAMDMMMWSPPTALVVSQQLRI 34
Db 307 SIYPGHITGHRAMDMMMWSPPTALVVAQLVRI 340

RESULT 18
PS0164
envelope glycoprotein (clone 64) - hepatitis C virus (fragment)
C:Species: hepatitis C virus
C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
C/Accession: PS0164
R:Hijikata, M.; Kato, N.; Ootsuyama, Y.; Nakagawa, M.; Okoshi, S.; Shimotohno, K.
Biochem. Biophys. Res. Commun. 175, 220-228, 1991
A>Title: Hypervariable regions in the putative glycoprotein of hepatitis C virus.
A:Reference number: FN0011; MUID:91151353; PMID:1847805
A:Accession: PS0164
A:Molecule type: genomic RNA
A:Residues: 1-315 <HIJ>
A:Cross-references: UNIPROT:Q00905; GB:D00690
A>Note: the authors translated the codon GAC for residues 27 and 112 as Gln
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: glycoprotein; polypeptide
F1200-209/Region: hypervariable 1 #status predicted
F1283-289/Region: hypervariable 2 #status predicted
F15,18,43,59,114,134,226,232,239,257,287/Binding site: carbohydrate (asn) (covalent) #st

Query Match 96.2%; Score 178; DB 2; Length 315;
Best Local Similarity 94.1%; Pred. No. 1.9e-17;
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRAMDMMMWSPPTALVVSQQLRI 34
Db 116 SIYPGHITGHRAMDMMMWSPPTALVVSQQLRI 149

RESULT 19
S18032
genome polypeptide - hepatitis C virus (isolate JK4) (fragment)
N:Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C:Species: hepatitis C virus
A:Variety: isolate JK4
C/Accession: S18032
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
R:Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A>Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
A:Reference number: S18029
A:Accession: S18032
A:Molecule type: genomic RNA
A:Residues: 1-782 <HON>

A/Cross-references: UNIPROT:Q68952; EMBL:X61594
 A/Experimental source: isolate JK4
 C/Superfamily: hepatitis C virus genome polypeptide
 C/Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
 F:1191/Product: core protein #status predicted <MAT1>
 F:192-383/Product: envelope protein 1 #status predicted <MAT2>
 F:384-733/Product: NS1/E2 protein #status predicted <MAT3>
 F:734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match 96.2%; Score 178; DB 2; Length 782;
 Best Local Similarity 91.2%; Pred. No. 5,3e-17;
 Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYGHITGHRMAMDMNMWSPPTALVVSQILRI 34
 DB 307 STYGHVSGHRMAMDMNMWSPPTALVVSQILRI 340

RESULT 20
 S18030
 genome polypeptide - hepatitis C virus (isolate JK1)
 N/Contains: capsid protein C; envelope protein M; hepatitis C virus (EC 3.4.21.98) (nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C/Species: hepatitis C virus
 A/Variety: isolate JK1
 C/Date: 19-May-2000 #sequence revision 19-May-2000 #text_change 09-Jul-2004
 C/Accession: S18030; S33570; A48332; S18029
 R/Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
 submitted to the EMBL Data Library, September 1991
 A/Description: A whole genome of hepatitis C virus cDNA was isolated from a single patient
 A/Reference number: S18028
 A/Accession: S18030
 A/Molecule type: genomic RNA
 A/Residues: 1-3010 <HON>

A/Cross-references: UNIPROT:Q68949; EMBL:X61596; NID:G59478; PIDN:CAA43793.1; PID:G59475
 A/Experimental source: isolate JK1 from an individual
 R/Honda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
 Arch. Virol. 128, 163-169, 1993

A/Title: Sequence analysis of putative structural regions of hepatitis C virus isolated
 A/Reference number: A48332; MID:93119270; PMID:8380322

A/Accession: S33570

A/Molecule type: genomic RNA

A/Residues: 1-547, 'T', 549-621, 'V', 623-624, 'S', 626-652, 'D', 655-761, 'T', 763-782 <HON>

A/Cross-references: EMBL:X61591

A/Note: this sequence is inconsistent with the nucleotide translation

A/Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 320

as Trp, and TTC for residue 771 as Ser

A/Note: sequence extracted from NCBI backbone (NCBIN:121747, NCBI:121748)

C/Superfamily: hepatitis C virus genome polypeptide

C/Keywords: ATP; glycoprotein; hydrolyase; nucleotide binding; P-loop; polypeptide; serin

F:2-115/Product: capsid protein C #status predicted <CPC>

F:116-191/Product: envelope protein M #status predicted <EPM>

F:192-389/Product: major envelope protein B #status predicted <MEB>

F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>

F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>

F:1007-1615/Product: hepatitis C virus #status predicted <NS3>

F:1202-1237/Region: nucleotide-binding motif A (P-loop)

F:1312-1317/Region: nucleotide-binding motif B

F:1316-1319/Region: DEXH motif

F:1616-1862/Product: nonstructural protein NS4a #status predicted <NS4a>

F:1863-2013/Product: nonstructural protein NS5 #status predicted <NS5>

F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>

F:196,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate (AG

Query Match 96.2%; Score 178; DB 1; Length 3010;
 Best Local Similarity 91.2%; Pred. No. 2.4e-16;
 Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYGHITGHRMAMDMNMWSPPTALVVSQILRI 34
 DB 307 STYGHVSGHRMAMDMNMWSPPTALVVSQILRI 340

RESULT 21
 A44150
 structural protein - hepatitis C virus

C/Species: hepatitis C virus

C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C/Accession: A44150

R/Ching, W.M.; Wyckowski, C.; Beach, M.J.; Wang, H.; Davies, C.L.; Carl, M.; Bradley, D.

Proc. Natl. Acad. Sci. U.S.A. 89, 3190-3194, 1992

A/Title: Interaction of immune sera with synthetic peptides corresponding to the structu

A/Reference number: A44150; MID:92228749; PMID:1373489

A/Accession: A44150

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: genomic RNA

A/Residues: 1-513 <CHI>

A/Cross-references: UNIPROT:Q91FE5; UNIPROT:Q36579; UNIPROT:Q36610; UNIPROT:Q9EL58; UNIP

C/Superfamily: hepatitis C virus genome polypeptide

Query Match 95.7%; Score 177; DB 2; Length 513;
 Best Local Similarity 94.1%; Pred. No. 4.6e-17;
 Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYGHITGHRMAMDMNMWSPPTALVVSQILRI 34
 DB 307 STYGHVSGHRMAMDMNMWSPPTALVVSQILRI 340

RESULT 22

S21471
 genome polypeptide - hepatitis C virus (fragment)

N/Contains: capsid protein; envelope protein

C/Species: hepatitis C virus

C/Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C/Accession: S21471

R/Mogam, W.K.
 submitted to the EMBL Data Library, April 1992

A/Reference number: S21471

A/Accession: S21471

A/Molecule type: genomic RNA

A/Residues: 1-369 <MOG>

A/Cross-references: UNIPROT:Q68869; EMBL:X65924; NID:G59466; PIDN:CAA46717.1; PID:G59467

C/Superfamily: hepatitis C virus genome polypeptide

C/Keywords: capsid protein; envelope protein; glycoprotein; polypeptide

Query Match 95.1%; Score 176; DB 2; Length 369;
 Best Local Similarity 93.9%; Pred. No. 4.4e-17;
 Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYGHITGHRMAMDMNMWSPPTALVVSQILRI 33
 DB 307 STYGHVSGHRMAMDMNMWSPPTALVVSQILRI 339

RESULT 23

S12707
 genome polypeptide - hepatitis C virus (fragment)

N/Contains: core protein; envelope protein

C/Species: hepatitis C virus

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: S12707

R/Takeuchi, K.; Kubo, Y.; Boonmar, S.; Watanabe, Y.; Katayama, T.; Choo, Q.L.; Kuo, G.

Nucleic Acids Res. 18, 4626, 1990

A/Title: Nucleotide sequence of core and envelope genes of the hepatitis C virus genome

A/Reference number: S12707; MID:90356432; PMID:2117749

A/Accession: S12707

A/Molecule type: genomic RNA

A/Residues: 1-441 <TKX>

A/Cross-references: UNIPROT:Q81776; EMBL:DD0574; NID:G221656; PIDN:BA00452.1; PID:G2216

C/Superfamily: hepatitis C virus genome polypeptide

C/Keywords: polypeptide

Query Match 94.8%; Score 175; DB 2; Length 441;
 Best Local Similarity 91.2%; Pred. No. 7.4e-17;
 Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Oy      1  SIYPGHITGHRMAMDMMNMNSPTTALVVSQLLRI 34
      |||:::|||||
Db      307 SIYPGHVSGHRMAMDMMNMNSPTTALVVSQLLRI 340

RESULT 24
J01925
polyprotein - hepatitis C virus (isolate HCV-KF)
N:Contains: C protein; E1 protein; E2/NS1 protein
C:Species: hepatitis C virus
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: J01925
R:Abel, K.; Inchausti, G.; Fujisawa, K.
J. Gen. Virol. 73, 2725-2729, 1992
A:Title: Genomic characterization and mutation rate of hepatitis C virus isolated from a
A:Reference number: J01925; MUID:93019030; PMID:1383400
A:Accession: J01925
A:Molecule type: mRNA
A:Residues: 1-520 <ABE>
A:Cross-references: UNIPROT:O01403; DBJ:D10687; NID:G221544; PIDN:BA01529.1; PID:G221544
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: polypeptide; transmembrane protein
F:1-191/Product: C protein #status predicted <CPR>
F:192-383/Product: E1 protein #status predicted <E1R>
F:384-520/Product: E2/NS1 protein #status predicted <E2P>

Query Match      94.6%; Score 175; DB 2; Length 520;
Best Local Similarity 91.2%; Pred. No. 8,9e-17;
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      1  SIYPGHITGHRMAMDMMNMNSPTTALVVSQLLRI 34
      |||:::|||||
Db      307 SIYPGHVSGHRMAMDMMNMNSPTTALVVSQLLRI 340

RESULT 25
S19875
genome polyprotein - hepatitis C virus (isolate JK3) (fragment)
N:Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C:Species: hepatitis C virus
A:Variety: isolate JK3
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S19875
R:Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A:Description: Sequence analysis of putative structural regions of Hepatitis C virus isolate
A:Reference number: S18029
A:Accession: S19875
A:Molecule type: genomic RNA
A:Residues: 1-782 <HON>
A:Cross-references: UNIPROT:O068951; EMBL:X61592; NID:G59482; PIDN:CAA43789.1; PID:G59483
A:Experimental source: isolate JK3
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
F:1-191/Product: core protein #status predicted <MAT1>
F:192-383/Product: envelope protein 1 #status predicted <MAT2>
F:384-733/Product: NS1/E2 protein #status predicted <MAT3>
F:734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match      94.1%; Score 174; DB 2; Length 782;
Best Local Similarity 94.1%; Pred. No. 2e-16;
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy      1  SIYPGHITGHRMAMDMMNMNSPTTALVVSQLLRI 34
      |||:::|||||
Db      307 SIYPGHVSGHRMAMDMMNMNSPTTALVVSQLLRI 340

genome polyprotein - hepatitis C virus
N:Contains: capsid protein C; envelope protein W; hepatitis A virus (EC 3.4.21.98) (nonstructural

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protein NS4a nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: S40770; P01285
R:Okamoto, H.
submitted to the EMBL Data Library, March 1992
A:Reference number: S40770
A:Accession: S40770
A:Molecule type: genomic RNA
A:Residues: 1-3011 <OKA>
A:Cross-references: UNIPROT:Q03463; EMBL:DI0749; NID:G221586; PIDN:BA01582.1, PID:G221586
R:Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda,
  Jpn. J. Exp. Med. 60, 167-177, 1990
A>Title: The 5'-terminal sequence of the hepatitis C virus genome.
A:Reference number: P01284; MUID:91013116; PMID:2170712
A:Accession: P01285
A:Molecule type: genomic RNA
A:Residues: 1-513 <OK2>
A:Cross-references: GB:D00831; NID:G221511; PIDN:BA00705.1; PID:G221512
A:Experimental source: isolate HC-J1
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: Arg; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin
F:2-115/Product: capsid protein C #status predicted <GPC>
F:116-191/Product: envelope protein M #status predicted <EM>
F:192-389/Product: major envelope protein E #status predicted <NEE>
F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F:1007-1615/Product: hepatitis virus #status predicted <NS3>
F:1230-1237/Region: nucleotide-binding motif A (P-loop)
F:1312-1317/Region: nucleotide-binding motif B
F:1316-1319/Region: DEXH motif
F:1616-1862/Product: nonstructural protein NS4a #status predicted <N4a>
F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4b>
F:2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>

Query Match          94.1%; Score 174; DB 1; Length 3011;
Best Local Similarity 91.2%; Pred. No. 6,8e-16;
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 STYPGHITGHRMADMMNWSPTALVVSQLLRI 34
DB 307 STYPGHITGHRMADMMNWSPTALVVSQLLRI 340

RESULT 27
PS0165
envelope glycoprotein (clone 168) - hepatitis C virus (fragment)
C:Species: hepatitis C virus
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
C:Accession: PS0165
R:Hiikata, M.; Kato, N.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Shimotohno, K.
Biochem. Biophys. Res. Commun. 175, 220-228, 1991
A>Title: Hypervariable regions in the putative glycoprotein of hepatitis C virus.
A:Reference number: F00011; MUID:91151353; PMID:1847805
A:Accession: PS0165
A:Molecule type: genomic RNA
A:Residues: 1-315 <HTJ>
A:Cross-references: UNIPROT:Q00906; GB:D00661
A>Note: the authors translated the codon GAC for residues 27 and 112 as Glu and CTT for
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: glycoprotein; polyprotein
F:200-209/Region: hypervariable 1 #status predicted
F:283-289/Region: hypervariable 2 #status predicted
F:516-59,114,134,226,232,239,257/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match          93.5%; Score 173; DB 2; Length 315;
Best Local Similarity 88.2%; Pred. No. 9,8e-17;
Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CY 1 STYPGHITGHRMADMMNWSPTALVVSQLLRI 34
DB 116 STYPGHITGHRMADMMNWSPTALVVSQLLRI 149

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RESULT 28

PC4407
envelope protein - hepatitis C virus (fragment)
C/Species: hepatitis C virus
C/Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004
C/Accession: PC4407
R/Li, G.; Yao, J.; Peng, W.
Chinese J. Virol. 13, 24-32, 1997
A/Title: Sequence of genomic region of hepatitis C virus envelope proteins from a Guang
A/Reference number: PC4407
A/Accession: PC4407
A/Molecule type: genomic RNA
A/Residues: 1-415 <LIA>
A/Cross-references: UNIPROT:Q7L2Y4
A/Note: the authors translated the codon ATA for residues 93 and 249 as Met
C/Superfamily: hepatitis C virus genome polypeptide
C/Keywords: envelope protein

Query Match 93.5%; Score 173; DB 2; Length 415;
Best Local Similarity 88.2%; Pred. No. 1,3e-16;
Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTALVVSQQLRI 34
DB 142 SIYPGHVSGHRMAMDMNMNSPTALVVSQQLRI 175

RESULT 29

J01926
polypeptide - hepatitis C virus (isolate HCV-476)
N/Contains: C protein; E1 protein; E2/NS1 protein
C/Species: hepatitis C virus
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C/Accession: J01926
R/Abbe, K.; Inchausti, G.; Fujisawa, K.
J. Gen. Virol. 73, 2725-2729, 1992
A/Title: Genomic characterization and mutation rate of hepatitis C virus isolated from a
A/Reference number: J01925; MUID:93019030; PMID:1383400
A/Accession: J01926
A/Molecule type: mRNA
A/Residues: 1-523 <ABE>
A/Cross-references: DDBJ:D10687
C/Superfamily: hepatitis C virus genome polypeptide
C/Keywords: polypeptide
F/1-191/Product: C protein #status predicted <CPR>
F/192-383/Product: E1 protein #status predicted <E1R>
F/384-523/Product: E2/NS1 protein #status predicted <E2P>

Query Match 93.5%; Score 173; DB 2; Length 523;
Best Local Similarity 88.2%; Pred. No. 1,7e-16;
Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTALVVSQQLRI 34
DB 307 SIYPGHVSGHRMAMDMNMNSPTALVVSQQLRI 340

RESULT 30

S19876
genome polypeptide - hepatitis C virus (isolate JKS) (fragment)
N/Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C/Species: hepatitis C virus
A/Variety: isolate JKS
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: S19876
R/Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A/Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
A/Reference number: S18029
A/Accession: S19876
A/Molecule type: genomic RNA
A/Residues: 1-782 <HON>

A/Cross-references: UNIPROT:Q68953; EMBL:X61595; NID:G59486; PIDN:CAA43792.1; PID:G59487
A/Experimental source: isolate JKS
C/Superfamily: hepatitis C virus genome polypeptide
C/Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
F/1-191/Product: core protein #status predicted <MA1>
F/192-383/Product: envelope protein 1 #status predicted <MA2>
F/384-733/Product: NS1/E2 protein #status predicted <MA3>
F/734-782/Product: nonstructural protein 2 (fragment) #status predicted <MA4>

Query Match 93.0%; Score 172; DB 2; Length 782;
Best Local Similarity 88.2%; Pred. No. 3,7e-16;
Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTALVVSQQLRI 34
DB 307 SIYPGHVSGHRMAMDMNMNSPTALVVSQQLRI 340

RESULT 31

GNWVCH
genome polypeptide - hepatitis C virus (strain H)
N/Contains: capsid protein C; envelope protein M; hepatitis virus (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C/Species: hepatitis C virus
A/Note: host Homo sapiens (man)
C/Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C/Accession: A36814; A41546
R/Inchausti, G.; Zebadee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
submitted to GenBank, July 1992
A/Description: Genomic structure of the human prototype strain H of hepatitis C virus: c
A/Reference number: A36814
A/Accession: A36814
A/Molecule type: genomic RNA
A/Residues: 1-3011 <INC>
A/Cross-references: UNIPROT:P27958; GB:M67463; NID:G329737; PIDN:AAA45534.1; PID:G329738
R/Inchausti, G.; Zebadee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991
A/Title: Genomic structure of the human prototype strain H of hepatitis C virus: compari
A/Reference number: A41546; MUID:92052256; PMID:1658800

A/Contents: annotation
A/Note: neither amino acid nor nucleotide sequence is given
C/Superfamily: hepatitis C virus genome polypeptide
C/Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
F/1-115/Product: capsid protein C #status predicted <CPC>
F/116-191/Product: envelope protein M #status predicted <EPM>
F/192-389/Product: major envelope protein E #status predicted <MEB>
F/390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F/730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F/1007-1615/Product: hepatitis virus #status predicted <NS3>
F/1230-1237/Region: nucleotide-binding motif A (P-loop)
F/1312-1317/Region: nucleotide-binding motif B
F/1316-1319/Region: DEXH motif

F/1616-1862/Product: nonstructural protein NS4a #status predicted <NS4>
F/1863-2013/Product: nonstructural protein NS4b #status predicted <NS5>
F/2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F/196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1215,1255,2041,2240,23

Query Match 93.0%; Score 172; DB 1; Length 3011;
Best Local Similarity 91.2%; Pred. No. 1,7e-15;
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTALVVSQQLRI 34
DB 307 SIYPGHITGHRMAMDMNMNSPTALVVSQQLRI 340

RESULT 32

S18031
genome polypeptide - hepatitis C virus (isolate J2) (fragment)
N/Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C/Species: hepatitis C virus
A/Variety: isolate J2
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C/Accession: S18031
 R/Honda, M.; Kaneko, S.; Masehi, U.; Kobayashi, K.; Murakami, S.
 Submitted to the EMBL Data Library, September 1991
 A/Description: Sequence analysis of putative structural regions of Hepatitis C Virus 1sc
 A/Reference number: S18029
 A/Accession: S18031
 A/Molecule type: genomic RNA
 A/Residues: 1-782 <MON>
 A/Cross-references: UNIPROT:Q68950; EMBL:X61593
 A/Experimental source: isolate UK2
 C/Superfamily: hepatitis C virus genome polypeptide
 C/Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
 F1-191/Product: core protein #status predicted <MAT1>
 F1-192-383/Product: envelope protein 1 #status predicted <MAT2>
 F1384-733/Product: NS1/E2 protein #status predicted <MAT3>
 F134-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match 91.9%; Score 170; DB 2; Length 782;
 Best Local Similarity 88.2%; Pred. No. 7, 2e-16;
 Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYGHITGHRMAMDMNMNSPTTALVVSQILRI 34
 Db 307 STYGHITGHRMAMDMNMNSPTTALVVSQILRI 340

RESULT 33

JC5620
 genome polypeptide - hepatitis C virus (isolate ETH480)
 N/Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
 protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C/Species: hepatitis C virus
 C/Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
 C/Accession: JC5620
 R/Chamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M.
 Biochem. Biophys. Res. Commun. 236, 44-49, 1997
 A/Title: The complete coding sequence of hepatitis C virus genotype 5a, the predominant
 A/Reference number: JC5620; MUID:9726593; PMID:9223423
 A/Accession: JC5620
 A/Molecule type: mRNA
 A/Residues: 1-3014 <CHRA>
 A/Cross-references: UNIPROT:Q39928; GB:Y13184
 A/Experimental source: genotype 5a, which predominates in South Africa
 A/Note: the translation of the nucleotide sequence is not complete in this paper
 C/Superfamily: hepatitis C virus genome polypeptide
 C/Keywords: ATP; glycoprotein; hydrolase; nucleic acid binding; P-loop; polypeptide; serin
 F1-115/Product: capsid protein C #status predicted <CPC>
 F116-191/Product: envelope protein M #status predicted <EPM>
 F1192-383/Product: major envelope protein E #status predicted <MEB>
 F1384-408/Region: hypervariable #status predicted
 F1390-733/Product: nonstructural protein NS1 #status predicted <NS1>
 F1731-1007/Product: nonstructural protein NS2 #status predicted <NS2>
 F11008-1616/Product: hepacivirin #status predicted <NS3>
 F11231-1238/Region: nucleotide-binding motif A (P-loop)
 F11313-1118/Region: nucleotide-binding motif B
 F11317-1320/Region: DEXH motif
 F11617-1863/Product: nonstructural protein NS4a #status predicted <N4A>
 F11864-2014/Product: nonstructural protein NS4b #status predicted <N4B>
 F12015-3014/Product: nonstructural protein NS5 #status predicted <NS5>
 F12210-2249/Region: interferon sensitivity determining #status predicted

Query Match 87.6%; Score 162; DB 1; Length 3014;
 Best Local Similarity 85.3%; Pred. No. 4, 4e-14;
 Matches 29; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STYGHITGHRMAMDMNMNSPTTALVVSQILRI 34
 Db 307 STYGHITGHRMAMDMNMNSPTTALVVSQILRI 340

RESULT 34
 S41288
 genome polypeptide - hepatitis C virus (fragment)

N/Contains: core protein; envelope protein; NS1 protein
 C/Species: hepatitis C virus
 C/Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: S41288
 R/Seliger, R.
 submitted to the EMBL Data Library, December 1993
 A/Reference number: S41288
 A/Accession: S41288
 A/Molecule type: genomic RNA
 A/Residues: 1-492 <SEB>
 A/Cross-references: UNIPROT:Q68870; EMBL:X76918
 C/Superfamily: hepatitis C virus genome polypeptide
 C/Keywords: capsid protein; core protein; envelope protein; nonstructural protein; poly
 F1-191/Product: core protein #status predicted <COR>
 F1192-372/Product: envelope protein #status predicted <ENV>
 F1373-492/Product: NS1 protein (fragment) #status predicted <NS1>

Query Match 81.6%; Score 151; DB 2; Length 492;
 Best Local Similarity 70.6%; Pred. No. 2e-13;
 Matches 24; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 STYGHITGHRMAMDMNMNSPTTALVVSQILRI 34
 Db 307 STYGHITGHRMAMDMNMNSPTTALVVSQILRI 340

RESULT 35

PC2060
 genome polypeptide N1 - hepatitis C virus
 N/Contains: envelope protein E1; nonstructural protein E2/NS1
 C/Species: hepatitis C virus
 C/Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
 C/Accession: PC2060
 R/Li, U.S.; Valtitski, L.; Tong, S.P.; Trepo, C.
 Biochem. Biophys. Res. Commun. 199, 1474-1481, 1994
 A/Title: Identification of the third major genotype of hepatitis C virus in France.
 A/Reference number: PC2060; MUID:94197744; PMID:8147893
 A/Accession: PC2060
 A/Molecule type: mRNA
 A/Residues: 1-411 <LIU>
 A/Cross-references: UNIPROT:Q81489
 C/Superfamily: hepatitis C virus genome polypeptide
 C/Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
 F1192-393/Product: envelope protein E1 #status predicted <EPE>
 F1364-411/Product: nonstructural protein E2/NS1 #status predicted <NPE>
 F1196-209,234,305,325/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 80.0%; Score 148; DB 2; Length 411;
 Best Local Similarity 67.6%; Pred. No. 4, 4e-13;
 Matches 23; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 STYGHITGHRMAMDMNMNSPTTALVVSQILRI 34
 Db 307 STYGHITGHRMAMDMNMNSPTTALVVSQILRI 340

RESULT 36
 PC2061
 genome polypeptide N2 - hepatitis C virus
 N/Contains: envelope protein E1; nonstructural protein E2/NS1
 C/Species: hepatitis C virus
 C/Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
 C/Accession: PC2061
 R/Li, U.S.; Valtitski, L.; Tong, S.P.; Trepo, C.
 Biochem. Biophys. Res. Commun. 199, 1474-1481, 1994
 A/Title: Identification of the third major genotype of hepatitis C virus in France.
 A/Reference number: PC2060; MUID:94197744; PMID:8147893
 A/Accession: PC2061
 A/Molecule type: mRNA
 A/Residues: 1-411 <LIU>
 A/Cross-references: UNIPROT:Q81813; GB:U12355; MUID:9410169; PIDN:AAA20155.1; PID:9410170
 C/Superfamily: hepatitis C virus genome polypeptide
 C/Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;

F:192-383/Product: envelope protein E1 #status predicted <SPE>
F:384-411/Product: nonstructural protein E2/NS1 #status predicted <NPE>
F:196,209,233,305,325/Binding site: carbonyldehydrate (Asn) (covalent) #status predicted

Query Match 80.0%; Score 148; DB 2; Length 411;
Best Local Similarity 67.6%; Pred. No. 4,4e-13;
Matches 23; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQQLRI 34
DB 307 SIYPGHITGHRMAMDMNMWSPPTALVVSQQLRI 340

RESULT 37
353630
genome polypeptide - hepatitis C virus (fragment)
N:Contains: envelope protein
C:Species: hepatitis C virus
C:Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 17-Nov-2000

C:Accession: J01303
R:Okamoto, H.; Okada, S.; Sugiyama, Y.; Kura, K.; Itzuka, H.; Machida, A.; Miyakawa, Y.
Nucleic Acids Res. 21, 1037, 1993
A:Title: Nucleotide sequence of the hepatitis C virus genome from a patient negative for
A:Reference number: J01303; PMID:8383835
A:Accession: J01303

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-193 <SAR>
A:Cross-references: EMBL:D13970
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: polypeptide
F:1-193/Product: envelope protein (fragment) #status predicted <MAT>

Query Match 79.5%; Score 147; DB 2; Length 193;
Best Local Similarity 70.6%; Pred. No. 2.6e-13;
Matches 24; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQQLRI 34
DB 117 SIYPGHITGHRMAMDMNMWSPPTALVVSQQLRI 150

RESULT 38
J00881
genome polypeptide - hepatitis C virus (strain J6) (fragments)
N:Contains: NS5 protein
C:Species: hepatitis C virus
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: J00881
R:Okamoto, H.

submitted to JIPD, January 1991
A:Description: The 5'-terminal and 3'-terminal sequences of the genomic RNA of hepatitis
A:Reference number: J00879
A:Accession: J00881
A:Molecule type: genomic RNA
A:Residues: 1-874 <OKA>
A:Cross-references: UNIPROT:Q7LZYS
A:Experimental source: strain J6
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: polypeptide
F:510-874/Product: NS5 protein (fragment) #status predicted <NS5>

Query Match 77.3%; Score 143; DB 2; Length 874;
Best Local Similarity 67.6%; Pred. No. 5.2e-12;
Matches 23; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQQLRI 34
DB 307 SIYPGHITGHRMAMDMNMWSPPTALVVSQQLRI 340

RESULT 39

J01303
genome polypeptide - hepatitis C virus (isolate HC-J6)
N:Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C:Species: hepatitis C virus
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: J01303
R:Okamoto, H.; Okada, S.; Sugiyama, Y.; Kura, K.; Itzuka, H.; Machida, A.; Miyakawa, Y.
J. Gen. Virol. 72, 2697-2704, 1991
A:Title: Nucleotide sequence of the genomic RNA of hepatitis C virus isolated from a hum
A:Reference number: J01303; PMID:9204440; PMID:1658195
A:Accession: J01303

A:Molecule type: genomic RNA
A:Residues: 1-3033 <OKA>
A:Cross-references: UNIPROT:P26660; GB:D00944; NID:G221650; PIRN:BA00792.1; PID:G221651
A:Experimental source: isolate HC-J6 from a Japanese individual
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: ATP; glycoprotein; hydrolase; P-loop; polypeptide; serine proteinase; trans
F:12-115/Product: capsid protein C #status predicted <CPC>
F:116-191/Product: envelope protein M #status predicted <EPW>
F:192-389/Product: major envelope protein E #status predicted <MEP>
F:350-733/Product: nonstructural protein NS1 #status predicted <NS1>
F:724-1010/Product: nonstructural protein NS2 #status predicted <NS2>
F:1011-1619/Product: hepacivirin #status predicted <NS3>
F:1316-1321/Region: nucleocapsid-binding motif B

F:1320-1323/Region: DEXH motif
F:1620-1866/Product: nonstructural protein NS4a #status predicted <NS4A>
F:1667-2017/Product: nonstructural protein NS4b #status predicted <NS4B>
F:2018-3033/Product: nonstructural protein NS5 #status predicted <NS5>
F:196,209,234,305,325,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038,28

Query Match 77.3%; Score 143; DB 1; Length 3033;
Best Local Similarity 67.6%; Pred. No. 2.1e-11;
Matches 23; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQQLRI 34
DB 307 SIYPGHITGHRMAMDMNMWSPPTALVVSQQLRI 340

RESULT 40
J00883
genome polypeptide - hepatitis C virus (strain J7) (fragments)
N:Contains: NS5 protein
C:Species: hepatitis C virus
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: J00883
R:Okamoto, H.

submitted to JIPD, January 1991
A:Description: The 5'-terminal and 3'-terminal sequences of the genomic RNA of hepatitis
A:Reference number: J00879
A:Accession: J00883
A:Molecule type: genomic RNA
A:Residues: 1-874 <OKA>
A:Cross-references: UNIPROT:Q7LZYS
A:Experimental source: strain J7
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: polypeptide
F:510-874/Product: NS5 protein (fragment) #status predicted <NS5>

Query Match 74.6%; Score 138; DB 2; Length 874;
Best Local Similarity 64.7%; Pred. No. 2.6e-11;
Matches 22; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQQLRI 34
DB 307 SIYPGHITGHRMAMDMNMWSPPTALVVSQQLRI 340

Search completed: November 10, 2004, 18:18:37
Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2004, 18:01:19 ; Search time 194 Seconds
(without alignments)
100.839 Million cell updates/sec

Title: US-10-685-435-15

Perfect score: 185
Sequence: 1 SIYPGHITGHRMAMDMMMSPTTALVVSQRLRI 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185	100.0	119	2	Q80NH1
2	185	100.0	119	2	Q80NK9
3	185	100.0	119	2	Q80NL0
4	185	100.0	119	2	Q80NM4
5	185	100.0	154	2	Q91615
6	185	100.0	154	2	Q91616
7	185	100.0	154	2	Q91619
8	185	100.0	154	2	Q91619
9	185	100.0	154	2	Q91619
10	185	100.0	154	2	Q91619
11	185	100.0	154	2	Q91619
12	185	100.0	154	2	Q91619
13	185	100.0	154	2	Q91619
14	185	100.0	154	2	Q91619
15	185	100.0	154	2	Q91619
16	185	100.0	154	2	Q91619
17	185	100.0	154	2	Q91619
18	185	100.0	154	2	Q91619
19	185	100.0	154	2	Q91619
20	185	100.0	154	2	Q91619
21	185	100.0	154	2	Q91619
22	185	100.0	154	2	Q91619
23	185	100.0	154	2	Q91619
24	185	100.0	154	2	Q91619
25	185	100.0	154	2	Q91619
26	185	100.0	154	2	Q91619
27	185	100.0	154	2	Q91619
28	185	100.0	154	2	Q91619
29	185	100.0	154	2	Q91619
30	185	100.0	154	2	Q91619
31	185	100.0	154	2	Q91619

32	184	99.5	119	2	Q80NN2
33	184	99.5	119	2	Q80NN3
34	184	99.5	154	2	Q91617
35	184	99.5	154	2	Q91617
36	184	99.5	154	2	Q91617
37	184	99.5	154	2	Q91617
38	184	99.5	154	2	Q91617
39	184	99.5	154	2	Q91617
40	184	99.5	154	2	Q91617
41	184	99.5	154	2	Q91617
42	184	99.5	154	2	Q91617
43	184	99.5	154	2	Q91617
44	184	99.5	154	2	Q91617
45	184	99.5	154	2	Q91617

ALIGNMENTS

```

RESULT 1
Q80NH1 PRELIMINARY; PRT; 119 AA.
AC Q80NH1;
DT 01-JUN-2003 (TEMBREL. 24, Created)
DT 01-JUN-2003 (TEMBREL. 24, Last sequence update)
DE Envelope protein EI (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2447295; PubMed=12560577;
RA Cantaloube J.F., Blagini P., Atout H., Gallian P., de Micco P.,
RA de Lamballerie X.;
RT "Evolution of hepatitis C virus in blood donors and their respective
RT recipients.";
RL J. Gen. Virol. 84:441-446(2003).
DR EMBL; AF15912; AAC83219.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR02519; HCV env.
DR Pfam; PF01539; HCV env; I.
KW Coat protein; Envelope protein; Glycoprotein; Polypeptide;
KW Transmembrane.
FT NON TER 1 1
FT NON TER 119 119
SQ SEQUENCE 119 AA; 13097 MW; 93A5C775F158D275 CRC64;

Query Match 100.0%; Score 185; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMMMSPTTALVVSQRLRI 34
Db 78 SIYPGHITGHRMAMDMMMSPTTALVVSQRLRI 111

RESULT 2
Q80NK9 PRELIMINARY; PRT; 119 AA.
AC Q80NK9;
DT 01-JUN-2003 (TEMBREL. 24, Created)
DT 01-JUN-2003 (TEMBREL. 24, Last sequence update)
DE Envelope protein EI (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22447295; PubMed=12560577;
RA Canaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
RA de Lamballerie X.;
RT "Evolution of hepatitis C virus in blood donors and their respective
RT recipients.";
RL J. Gen. Virol. 84:441-446(2003).
DR EMBL: AF515874; AAC8318.1; -.
DR GO:GO:0016021; C:integral to membrane; IEA.
DR GO:GO:0019028; C:viral capsid; IEA.
DR GO:GO:0019031; C:viral envelope; IEA.
DR GO:GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR002519; HCV env.
DR Pfam: PF01539; HCV env; I.
KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER 1
FT TER 119
SQ SEQUENCE 119 AA; 13220 MW; 96446D861A8C5AD CRC64;

```

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Query Match
Best Local Similarity 100.0%; Score 185; DB 2; Length 119;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 SIYPGHITGHRMAMDMNMMSPTTALVVSQILRI 34
Db 78 SIYPGHITGHRMAMDMNMMSPTTALVVSQILRI 111

```

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RESULT 3
Q80N10 PRELIMINARY; PRT; 119 AA.
AC Q80N10;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DS Envelope protein E1 (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_Taxid=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22447295; PubMed=12560577;
RA Canaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
RA de Lamballerie X.;
RT "Evolution of hepatitis C virus in blood donors and their respective
RT recipients.";
RL J. Gen. Virol. 84:441-446(2003).
DR EMBL: AF515873; AAC83180.1; -.
DR GO:GO:0016021; C:integral to membrane; IEA.
DR GO:GO:0019028; C:viral capsid; IEA.
DR GO:GO:0019031; C:viral envelope; IEA.
DR GO:GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR002519; HCV env.
DR Pfam: PF01539; HCV env; I.
KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER 1
FT TER 119
SQ SEQUENCE 119 AA; 13220 MW; 06498FCD7720B5B2 CRC64;

```

```

Query Match
Best Local Similarity 100.0%; Score 185; DB 2; Length 119;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 SIYPGHITGHRMAMDMNMMSPTTALVVSQILRI 34
Db 78 SIYPGHITGHRMAMDMNMMSPTTALVVSQILRI 111

```

RESULT 4

```

Q80NN4 PRELIMINARY; PRT; 119 AA.
AC Q80NN4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DS Envelope protein E1 (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_Taxid=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22447295; PubMed=12560577;
RA Canaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
RA de Lamballerie X.;
RT "Evolution of hepatitis C virus in blood donors and their respective
RT recipients.";
RL J. Gen. Virol. 84:441-446(2003).
DR EMBL: AF515849; AAC83156.1; -.
DR GO:GO:0016021; C:integral to membrane; IEA.
DR GO:GO:0019028; C:viral capsid; IEA.
DR GO:GO:0019031; C:viral envelope; IEA.
DR GO:GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR002519; HCV env.
DR Pfam: PF01539; HCV env; I.
KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER 1
FT TER 119
SQ SEQUENCE 119 AA; 13130 MW; 347C2477AD8E1568 CRC64;

```

```

Query Match
Best Local Similarity 100.0%; Score 185; DB 2; Length 119;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 SIYPGHITGHRMAMDMNMMSPTTALVVSQILRI 34
Db 78 SIYPGHITGHRMAMDMNMMSPTTALVVSQILRI 111

```

```

RESULT 5
Q91615 PRELIMINARY; PRT; 154 AA.
AC Q91615;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DS Polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_Taxid=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22291660; PubMed=12404223;
RA Lyra A.C., Fan X., Lang D.M., Yustin K., Ramrakhiani S., Brunt E.M.,
RA Korber B., Fereyson A.S., Di Bisceglie A.M.;
RT "Evolution of hepatitis C viral quasispecies after liver
RT transplantation.";
RL Gastroenterology 123:1485-1493(2002).
DR EMBL: AF422464; AA12476.1; -.
DR GO:GO:0016021; C:integral to membrane; IEA.
DR GO:GO:0019028; C:viral capsid; IEA.
DR GO:GO:0019031; C:viral envelope; IEA.
DR GO:GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR002519; HCV env.
DR InterPro: IPR002531; HCV NS1.
DR Pfam: PF01539; HCV env; I.
DR Pfam: PF01560; HCV NS1; I.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT TER 1

```

FT CHAIN <1 >154 envelope glycoprotein EI/E2.
 FT NON_TER 154
 SQ SEQUENCE 154 AA; 16718 MW; 0FECA0FB07B2513C CRC64;

Query Match
 Best Local Similarity 100.0%; Score 185; DB 2; Length 154;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 34
 DB 22 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 55

RESULT 6

ID Q91616 PRELIMINARY; PRT; 154 AA.
 AC Q91616;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Polypeptide (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22291660; PubMed=12404223;
 RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramakrishni S., Brunt E.M.,
 RA Korber B., Peterson A.S., Di Bisceglie A.M.;
 RT "Evolution of hepatitis C viral quasispecies after liver
 RT transplantation.";
 RL Gastroenterology 123:1485-1493(2002).
 DR EMBL; AF422463; ALU24775.1; -.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env.
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01539; HCV_env; I.
 DR Pfam; PF01560; HCV_NSI; I.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polypeptide; Transmembrane.
 FT NON_TER 1 154
 FT CHAIN <1 >154 envelope glycoprotein EI/E2.
 FT NON_TER 154 154
 SQ SEQUENCE 154 AA; 16733 MW; 420ABD231D02469A CRC64;

Query Match
 Best Local Similarity 100.0%; Score 185; DB 2; Length 154;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 34
 DB 22 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 55

RESULT 7

ID Q91619 PRELIMINARY; PRT; 154 AA.
 AC Q91619;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Polypeptide (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22291660; PubMed=12404223;

RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramakrishni S., Brunt E.M.,
 RA Korber B., Peterson A.S., Di Bisceglie A.M.;
 RT "Evolution of hepatitis C viral quasispecies after liver
 RT transplantation.";
 RL Gastroenterology 123:1485-1493(2002).
 DR EMBL; AF422463; ALU24775.1; -.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env.
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01539; HCV_env; I.
 DR Pfam; PF01560; HCV_NSI; I.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polypeptide; Transmembrane.
 FT NON_TER 1 154
 FT CHAIN <1 >154 envelope glycoprotein EI/E2.
 FT NON_TER 154 154
 SQ SEQUENCE 154 AA; 16703 MW; 5E7ABD230817468F CRC64;

Query Match
 Best Local Similarity 100.0%; Score 185; DB 2; Length 154;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 34
 DB 22 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 55

RESULT 8

ID Q91620 PRELIMINARY; PRT; 154 AA.
 AC Q91620;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Polypeptide (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22291660; PubMed=12404223;
 RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramakrishni S., Brunt E.M.,
 RA Korber B., Peterson A.S., Di Bisceglie A.M.;
 RT "Evolution of hepatitis C viral quasispecies after liver
 RT transplantation.";
 RL Gastroenterology 123:1485-1493(2002).
 DR EMBL; AF422459; ALU24771.1; -.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env.
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01539; HCV env; I.
 DR Pfam; PF01560; HCV_NSI; I.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polypeptide; Transmembrane.
 FT NON_TER 1 154
 FT CHAIN <1 >154 envelope glycoprotein EI/E2.
 FT NON_TER 154 154
 SQ SEQUENCE 154 AA; 16703 MW; 5E7ABD230817468F CRC64;

Query Match
 Best Local Similarity 100.0%; Score 185; DB 2; Length 154;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 34
 DB 22 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 55

RESULT 9

Q916J3 PRELIMINARY; PRT; 154 AA.

AC Q916J3; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Polypeptide (Fragment).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

OX NCBI_TaxID=11103;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22291660; PubMed=12404223;

RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramrakhiani S., Brunt E.M., Korber B., Perelson A.S., Di Bisceglie A.M.; "Evolution of hepatitis C viral quasispecies after liver transplantation."

RT Gastroenterology 123:1485-1493 (2002).

RL EMBL: AF422456; AAL24768.1; -

DR GO:0016021; C:integral to membrane; IEA.

DR GO:0019028; C:viral capsid; IEA.

DR GO:0019031; F:structural molecule activity; IEA.

DR InterPro: IPR002519; HCV env.

DR InterPro: IPR002531; HCV NS1.

DR Pfam: PF01539; HCV env; 1.

DR Pfam: PF01560; HCV NS1; 1.

KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polypeptide; Transmembrane.

KW NON TER 1

FT CHAIN <1 >154 envelope glycoprotein E1/E2.

FT NON TER 154 154

SO SEQUENCE 154 AA; 16732 MW; 84EF18C0840C2122 CRC64;

Query Match 100.0%; Score 185; DB 2; Length 154;

Best Local Similarity 100.0%; Pred. No. 1.4e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMNSPTTALVVSQILRI 34
 |||||
 DB 22 SIYPGHITGHRAMDMNMNSPTTALVVSQILRI 55

RESULT 10

Q916J4 PRELIMINARY; PRT; 154 AA.

AC Q916J4; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Polypeptide (Fragment).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

OX NCBI_TaxID=11103;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22291660; PubMed=12404223;

RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramrakhiani S., Brunt E.M., Korber B., Perelson A.S., Di Bisceglie A.M.; "Evolution of hepatitis C viral quasispecies after liver transplantation."

RT Gastroenterology 123:1485-1493 (2002).

RL EMBL: AF422455; AAL24767.1; -

DR GO:0016021; C:integral to membrane; IEA.

DR GO:0019028; C:viral capsid; IEA.

DR GO:0019031; F:structural molecule activity; IEA.

DR InterPro: IPR002519; HCV env.

DR InterPro: IPR002531; HCV NS1.

DR Pfam: PF01539; HCV env; 1.

DR Pfam: PF01560; HCV NS1; 1.

KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polypeptide; Transmembrane.

KW NON TER 1

FT CHAIN <1 >154 envelope glycoprotein E1/E2.

FT NON TER 154 154

SO SEQUENCE 154 AA; 16732 MW; 84EF18C0840C2122 CRC64;

Query Match 100.0%; Score 185; DB 2; Length 154;

Best Local Similarity 100.0%; Pred. No. 1.4e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMNSPTTALVVSQILRI 34
 |||||
 DB 22 SIYPGHITGHRAMDMNMNSPTTALVVSQILRI 55

RESULT 11

Q916J6 PRELIMINARY; PRT; 154 AA.

AC Q916J6; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Polypeptide (Fragment).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

OX NCBI_TaxID=11103;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22291660; PubMed=12404223;

RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramrakhiani S., Brunt E.M., Korber B., Perelson A.S., Di Bisceglie A.M.; "Evolution of hepatitis C viral quasispecies after liver transplantation."

RT Gastroenterology 123:1485-1493 (2002).

RL EMBL: AF422453; AAL24765.1; -

DR GO:0016021; C:integral to membrane; IEA.

DR GO:0019028; C:viral capsid; IEA.

DR GO:0019031; F:structural molecule activity; IEA.

DR InterPro: IPR002519; HCV env.

DR InterPro: IPR002531; HCV NS1.

DR Pfam: PF01539; HCV env; 1.

DR Pfam: PF01560; HCV NS1; 1.

KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polypeptide; Transmembrane.

KW NON TER 1

FT CHAIN <1 >154 envelope glycoprotein E1/E2.

FT NON TER 154 154

SO SEQUENCE 154 AA; 16732 MW; 84EF18C0840C2122 CRC64;

Query Match 100.0%; Score 185; DB 2; Length 154;

Best Local Similarity 100.0%; Pred. No. 1.4e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRAMDMNMNSPTTALVVSQILRI 34
 |||||
 DB 22 SIYPGHITGHRAMDMNMNSPTTALVVSQILRI 55

RESULT 12

Q916J7 PRELIMINARY; PRT; 154 AA.

AC Q916J7; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Polypeptide (Fragment).

OS Hepatitis C virus.

```

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OK NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22291660; PubMed=12404223;
RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramrakhiani S., Brunt E.M.,
RT "Evolution of hepatitis C viral quasispecies after liver
transplantation."
RL Gastroenterology 123:1485-1493(2002).
DR EMBL; AF422452; AAL24764.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002519; HCV env.
DR Pfam; PF01539; HCV_NSI.
DR Pfam; PF01560; HCV_NSI; 1.
DR Coats protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT CHAIN <1 >154 envelope glycoprotein E1/E2.
FT NON_TER 154
SQ SEQUENCE 154 AA; 16733 MW; 420ABD231D02469A CRC64;

Query Match 100.0%; Score 185; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 1,4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
Db 22 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 55

RESULT 13
Q916J8 PRELIMINARY; PRT; 154 AA.
AC Q916J8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22291660; PubMed=12404223;
RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramrakhiani S., Brunt E.M.,
RT "Evolution of hepatitis C viral quasispecies after liver
transplantation."
RL Gastroenterology 123:1485-1493(2002).
DR EMBL; AF422451; AAL24763.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01539; HCV env; 1.
DR Pfam; PF01560; HCV_NSI; 1.
DR Coats protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT CHAIN <1 >154 envelope glycoprotein E1/E2.
FT NON_TER 154
SQ SEQUENCE 154 AA; 16702 MW; B7EFD0D3640C213C CRC64;

Query Match 100.0%; Score 185; DB 2; Length 154;

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```

Best Local Similarity 100.0%; Pred. No. 1,4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
Db 22 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 55

RESULT 14
Q8QOE7 PRELIMINARY; PRT; 154 AA.
AC Q8QOE7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E1/E2 protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22291660; PubMed=12404223;
RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramrakhiani S., Brunt E.M.,
RT "Evolution of hepatitis C viral quasispecies after liver
transplantation."
RL Gastroenterology 123:1485-1493(2002).
DR EMBL; AF497393; AAM19646.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01539; HCV env; 1.
DR Pfam; PF01560; HCV_NSI; 1.
DR Coats protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 16704 MW; D2E87A1E30C3753 CRC64;

Query Match 100.0%; Score 185; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 1,4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
Db 22 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 55

RESULT 15
Q8QOE8 PRELIMINARY; PRT; 154 AA.
AC Q8QOE8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E1/E2 protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22291660; PubMed=12404223;
RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramrakhiani S., Brunt E.M.,
RT "Evolution of hepatitis C viral quasispecies after liver
transplantation."
RL Gastroenterology 123:1485-1493(2002).
DR EMBL; AF497392; AAM19646.1; -.

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DR GO:0016021; C: integral to membrane; IEA.
DR GO:0019028; C: viral capsid; IEA.
DR GO:0019031; C: viral envelope; IEA.
DR GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR002519; HCV Env.
DR InterPro: IPR002531; HCV NS1.
DR Pfam: PF01539; HCV env; 1.
DR Pfam: PF01560; HCV NS1; 1.
DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 16732 MW; 84EF18C0840C2122 CRC64;

Query Match 100.0%; Score 185; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 1,4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34
Db 22 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 55

RESULT 16
Q8QOE9 PRELIMINARY; PRT; 154 AA.
AC Q8QOE9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E1/22 protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_Taxid=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22291660; PubMed=12404223;
RA Lyra A.C., Fan X., Tang D.M., Yusim K., Ramrakhiani S., Brunt E.M.,
Korber B., Perelson A.S., Di Bisceglie A.M.,
RT "Evolution of hepatitis C viral quasispecies after liver
transplantation.";
RT Gastroenterology 123:1485-1493(2002).
DR EMBL: AF497391; AAC19645.1;
DR GO:0016021; C: integral to membrane; IEA.
DR GO:0019028; C: viral capsid; IEA.
DR GO:0019031; C: viral envelope; IEA.
DR GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR002519; HCV env.
DR InterPro: IPR002531; HCV NS1.
DR Pfam: PF01539; HCV env; 1.
DR Pfam: PF01560; HCV NS1; 1.
DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 16732 MW; 84EF18C0840C2122 CRC64;

Query Match 100.0%; Score 185; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 1,4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34
Db 22 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 55

RESULT 17
Q81760 PRELIMINARY; PRT; 3010 AA.
AC Q81760;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_Taxid=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93359897; PubMed=8394876;
RA Wang Y., Okamoto H., Tsuba F., Nagayama R., Tao Q.M., Mishiro S.,
RT "Prevalence, genotypes, and an isolate (HC-C2) of hepatitis C virus in
Chinese patients with liver disease.";
RT J. Med. Virol. 40:254-260(1993).
RL U. Med. Virol. 40:254-260(1993).
DR EMBL: D10934; BAA01728.1;
DR PIR: A61196; A61196.
DR PIR: P0246; P0246.
DR PIR: P0254; P0254.
DR PIR: P0804; P0804.
DR PIR: P80329; P80329.
DR HSP: P26663; 10TV.

DR GO:0016021; C: integral to membrane; IEA.
DR GO:0019028; C: viral capsid; IEA.
DR GO:0019031; C: viral envelope; IEA.
DR GO:000524; F: ATP binding; IEA.
DR GO:0008026; F: ATP-dependent helicase activity; IEA.
DR GO:0003723; F: RNA binding; IEA.
DR GO:0003968; F: RNA-directed RNA polymerase activity; IEA.
DR GO:0008236; F: serine-type peptidase activity; IEA.
DR GO:0005198; F: structural molecule activity; IEA.
DR GO:0006508; P: proteolysis and peptidolysis; IEA.
DR GO:0006350; P: translation; IEA.
DR GO:0019079; P: viral genome replication; IEA.
DR GO:0019087; P: viral transformation; IEA.
DR InterPro: IPR000345; CytC_heme_BS.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR002522; HCV_capsid.
DR InterPro: IPR002521; HCV_core.
DR InterPro: IPR002519; HCV env.
DR InterPro: IPR002531; HCV NS1.
DR InterPro: IPR000745; HCV NS4a.
DR InterPro: IPR001480; HCV NS4b.
DR InterPro: IPR002868; HCV NS5a.
DR InterPro: IPR002166; HCV NS5a.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR004109; Helicase_S29.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR InterPro: IPR002518; Pept_U9_HCV_NS2.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR007094; RNA_pol_PSVir.
DR Pfam: PF01543; HCV capsid; 1.
DR Pfam: PF01542; HCV core; 1.
DR Pfam: PF01539; HCV env; 1.
DR Pfam: PF01560; HCV NS1; 1.
DR Pfam: PF01538; HCV NS2; 1.
DR Pfam: PF02907; HCV NS3; 1.
DR Pfam: PF01006; HCV NS4a; 1.
DR Pfam: PF01001; HCV NS4b; 1.
DR Pfam: PF01506; HCV NS5a; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF00998; Viral RdRp; 1.
DR SMART: SM00487; DEXDC; 1.
DR POSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
SQ SEQUENCE 3010 AA; 326857 MW; EA7D306A4BA2E224 CRC64;

Query Match 100.0%; Score 185; DB 2; Length 3010;
Best Local Similarity 100.0%; Pred. No. 3e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 34
Db 307 SIYPGHITGHRMAMDMNMWSPPTALVVSQLLRI 340

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RESULT 18
Q80NC7 PRELIMINARY; PRT; 119 AA.
ID Q80NC7
AC Q80NC7;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DE Envelope protein EI (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_Taxid=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22447295; PubMed=12560577;
RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
de Lamballerie X.;
RT "Evolution of hepatitis C virus in blood donors and their respective
recipients.";
RL J. Gen. Virol. 84:441-446(2003).
DR EMBL; AF515956; AA083263.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002519; HCV_env.
DR Pfam; PF01539; HCV_env; I.
KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13164 MW; 7C838FCF88D31EC1 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119;
Best Local Similarity 97.1%; Pred. No. 1.5e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 34
Db 78 SIYPGHVTHGRMAMDMNMWSPPTALVVSQILRI 111

RESULT 19
Q80ND3 PRELIMINARY; PRT; 119 AA.
ID Q80ND3
AC Q80ND3;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Envelope protein EI (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_Taxid=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22447295; PubMed=12560577;
RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
de Lamballerie X.;
RT "Evolution of hepatitis C virus in blood donors and their respective
recipients.";
RL J. Gen. Virol. 84:441-446(2003).
DR EMBL; AF515950; AA083257.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002519; HCV_env.
DR Pfam; PF01539; HCV_env; I.
KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13164 MW; 7C838FCF88D31EC1 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119;
Best Local Similarity 97.1%; Pred. No. 1.5e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 34
Db 78 SIYPGHVTHGRMAMDMNMWSPPTALVVSQILRI 111

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FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13252 MW; 6C583E1707341120 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119;
Best Local Similarity 97.1%; Pred. No. 1.5e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 34
Db 78 SIYPGHVTHGRMAMDMNMWSPPTALVVSQILRI 111

RESULT 20
Q80NH2 PRELIMINARY; PRT; 119 AA.
ID Q80NH2
AC Q80NH2;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Envelope protein EI (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_Taxid=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22447295; PubMed=12560577;
RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
de Lamballerie X.;
RT "Evolution of hepatitis C virus in blood donors and their respective
recipients.";
RL J. Gen. Virol. 84:441-446(2003).
DR EMBL; AF515911; AA083218.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002519; HCV_env.
DR Pfam; PF01539; HCV_env; I.
KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13091 MW; 789E31FCB22E7F10 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119;
Best Local Similarity 97.1%; Pred. No. 1.5e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 34
Db 78 SIYPGHVTHGRMAMDMNMWSPPTALVVSQILRI 111

RESULT 21
Q80NH9 PRELIMINARY; PRT; 119 AA.
ID Q80NH9
AC Q80NH9;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Envelope protein EI (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_Taxid=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22447295; PubMed=12560577;
RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
de Lamballerie X.;
RT "Evolution of hepatitis C virus in blood donors and their respective
recipients.";
RL J. Gen. Virol. 84:441-446(2003).
DR EMBL; AF515950; AA083257.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002519; HCV_env.
DR Pfam; PF01539; HCV_env; I.
KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13091 MW; 789E31FCB22E7F10 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119;
Best Local Similarity 97.1%; Pred. No. 1.5e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHITGHRMAMDMNMWSPPTALVVSQILRI 34
Db 78 SIYPGHVTHGRMAMDMNMWSPPTALVVSQILRI 111

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RT recipients.";
 RL U. Gen. Virol. 84:441-446(2003).
 DR EMBL; AF515904; AA083211.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV_env.
 DR Pfam; PF01539; HCV_env; I.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON_TER 1
 FT TER 119
 SQ SEQUENCE 119 AA; 13049 MW; 09E85D2052E0D3B1 CRC64;
 Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 22
 Q80N10 PRELIMINARY; PRT; 119 AA.
 ID Q80N10;
 AC Q80N10;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Envelope protein E1 (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22447295; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 RA "Evolution of hepatitis C virus in blood donors and their respective
 RT recipients.";
 RL U. Gen. Virol. 84:441-446(2003).
 DR EMBL; AF515903; AA083210.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV_env.
 DR Pfam; PF01539; HCV_env; I.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON_TER 1
 FT TER 119
 SQ SEQUENCE 119 AA; 13136 MW; D8127F49D4FBBC48 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPGHITGRMAMDMNMMSPTTLVVSQRLRI 34
 DB 78 STPGHVTGRMAMDMNMMSPTTLVVSQRLRI 111

RESULT 23
 Q80N12 PRELIMINARY; PRT; 119 AA.
 ID Q80N12;
 AC Q80N12;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Envelope protein E1 (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22447295; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 RA "Evolution of hepatitis C virus in blood donors and their respective
 RT recipients.";
 RL U. Gen. Virol. 84:441-446(2003).
 DR EMBL; AF515901; AA083208.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV_env.
 DR Pfam; PF01539; HCV_env; I.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON_TER 1
 FT TER 119
 SQ SEQUENCE 119 AA; 13171 MW; 644E689393A9FA41 CRC64;
 Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 24
 Q80N14 PRELIMINARY; PRT; 119 AA.
 ID Q80N14;
 AC Q80N14;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Envelope protein E1 (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22447295; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 RA "Evolution of hepatitis C virus in blood donors and their respective
 RT recipients.";
 RL U. Gen. Virol. 84:441-446(2003).
 DR EMBL; AF515889; AA083196.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV_env.
 DR Pfam; PF01539; HCV_env; I.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON_TER 1
 FT TER 119
 SQ SEQUENCE 119 AA; 13080 MW; 18002AD91EB0D7F9 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPGHITGRMAMDMNMMSPTTLVVSQRLRI 34

Db 78 SIYPGHVTHGRVAMDMNMNSPTTALVVSQQLRI 111

RESULT 25

Q80NK5 PRELIMINARY; PRT; 119 AA.
 ID Q80NK5; 080NK5;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Envelope protein E1 (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22447295; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 RA "Evolution of hepatitis C virus in blood donors and their respective
 RT recipients.";
 RL J. Gen. Virol. 84:441-446(2003).
 DR EMBL; AF515888; AA083185.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env; I.
 DR Pfam; PF01539; HCV env; I.
 KM Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13096 MW; 01FE4B9C16B0D3AC CRC64;
 Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 26

Q80NK4 PRELIMINARY; PRT; 119 AA.
 ID Q80NK4; 080NK4;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Envelope protein E1 (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22447295; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 RA "Evolution of hepatitis C virus in blood donors and their respective
 RT recipients.";
 RL J. Gen. Virol. 84:441-446(2003).
 DR EMBL; AF515879; AA083186.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env; I.
 DR Pfam; PF01539; HCV env; I.

KM Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13168 MW; 833357A8A2D8AA4 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHVTHGRVAMDMNMNSPTTALVVSQQLRI 34
 Db 78 SIYPGHVTHGRVAMDMNMNSPTTALVVSQQLRI 111

RESULT 27

Q80NK5 PRELIMINARY; PRT; 119 AA.
 ID Q80NK5; 080NK5;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Envelope protein E1 (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22447295; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
 RA "Evolution of hepatitis C virus in blood donors and their respective
 RT recipients.";
 RL J. Gen. Virol. 84:441-446(2003).
 DR EMBL; AF515878; AA083185.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env; I.
 DR Pfam; PF01539; HCV env; I.
 KM Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13182 MW; 08B0EF9328861ABA CRC64;
 Query Match 99.5%; Score 184; DB 2; Length 119;
 Best Local Similarity 97.1%; Pred. No. 1.5e-17;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SIYPGHVTHGRVAMDMNMNSPTTALVVSQQLRI 34
 Db 78 SIYPGHVTHGRVAMDMNMNSPTTALVVSQQLRI 111

RESULT 28

Q80NK6 PRELIMINARY; PRT; 119 AA.
 ID Q80NK6; 080NK6;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Envelope protein E1 (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22447295; PubMed=12560577;
 RA Cantaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,


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Qy      1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
      |||
Db      78 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRV 111

RESULT 32
Q80NN2  PRELIMINARY;      PRT;      119 AA.
AC      Q80NN2;
DT      01-JUN-2003 (TREMBLrel. 24, Created)
DT      01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DE      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Envelope protein E1 (Fragment).
OS      Hepatitis C virus.
OC      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC      Hepacivirus.
OX      NCBI_TaxId=11103;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22447295; PubMed=12560577;
RA      Canaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
RA      de Lamballerie X.;
RT      "Evolution of hepatitis C virus in blood donors and their respective
RT      recipients."
RL      J. Gen. Virol. 84:441-446(2003).
DR      EMBL; AF515851; AAO83158.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0019028; C:viral capsid; IEA.
DR      GO; GO:0039031; C:viral envelope; IEA.
DR      GO; GO:0005198; F:structural molecule activity; IEA.
DR      InterPro; IPR002519; HCV env.
DR      Pfam; PF01539; HCV env; 1.
DR      Coat protein; Envelope protein; Glycoprotein; Polyprotein;
DR      Transmembrane.
KW      NON TER
FT      NON TER
FT      SEQUENCE
SQ      119 AA; 13144 MW; 1F0EC961F9A8570C CRC64;

Query Match
Best Local Similarity 99.5%; Score 184; DB 2; Length 119;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
      |||
Db      78 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRV 111

RESULT 33
Q80NN3  PRELIMINARY;      PRT;      119 AA.
AC      Q80NN3;
DT      01-JUN-2003 (TREMBLrel. 24, Created)
DT      01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Envelope protein E1 (Fragment).
OS      Hepatitis C virus.
OC      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC      Hepacivirus.
OX      NCBI_TaxId=11103;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22447295; PubMed=12560577;
RA      Canaloube J.F., Biagini P., Attoui H., Gallian P., de Micco P.,
RA      de Lamballerie X.;
RT      "Evolution of hepatitis C virus in blood donors and their respective
RT      recipients."
RL      J. Gen. Virol. 84:441-446(2003).
DR      EMBL; AF515850; AAO83157.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0019028; C:integral to membrane; IEA.
DR      GO; GO:0019031; C:viral envelope; IEA.
DR      GO; GO:0005198; F:structural molecule activity; IEA.
DR      GO; GO:0005198; F:structural molecule activity; IEA.
```

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DR      InterPro; IPR002519; HCV env.
DR      Pfam; PF01539; HCV env; 1.
KW      Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW      Transmembrane.
FT      NON TER
FT      NON TER
FT      SEQUENCE
SQ      119 AA; 13144 MW; 1F0EC961F9A8570C CRC64;

Query Match
Best Local Similarity 99.5%; Score 184; DB 2; Length 119;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
      |||
Db      78 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRV 111

RESULT 34
Q916C1  PRELIMINARY;      PRT;      154 AA.
AC      Q916C1;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE      Polyprotein (Fragment).
OS      Hepatitis C virus.
OC      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC      Hepacivirus.
OX      NCBI_TaxId=11103;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22291660; PubMed=12404223;
RA      Lyra A.C., Fan X., Lang D.M., Yasim K., Ramrakhiani S., Brunt E.M.,
RA      Korber B., Petersen A.S., Di Biaseglio A.M.;
RT      "Evolution of hepatitis C viral quasispecies after liver
RT      transplantation."
RL      Gastroenterology 123:1485-1493(2002).
DR      EMBL; AF422458; ALN24770.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0019028; C:viral capsid; IEA.
DR      GO; GO:0019031; C:viral envelope; IEA.
DR      GO; GO:0005198; F:structural molecule activity; IEA.
DR      InterPro; IPR002531; HCV env.
DR      Pfam; PF01539; HCV env; 1.
DR      Pfam; PF01560; HCV NS1; 1.
KW      Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW      Polyprotein; Transmembrane.
FT      NON TER
FT      NON TER
FT      CHAIN
FT      NON TER
FT      SEQUENCE
SQ      154 AA; 16688 MW; 6DD398C02BF9907 CRC64;

Query Match
Best Local Similarity 99.5%; Score 184; DB 2; Length 154;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRI 34
      |||
Db      22 SIYPGHITGHRMAMDMNMNSPTTALVVSQLLRV 55

RESULT 35
Q916C2  PRELIMINARY;      PRT;      154 AA.
AC      Q916C2;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE      Polyprotein (Fragment).
OS      Hepatitis C virus.
OC      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC      Hepacivirus.
```

OX	NCBI_TaxID=11103;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=2229160; PubMed=12404223;
RA	Lya A.C., Fan X., Lang D.M., Yustin K., Ramrakhtiani S., Brunt E.M.,
RA	Korber B., Perelson A.S., Di Bisceglie A.M.;
RT	"Evolution of hepatitis C viral quasispecies after liver
RT	transplantation";
RL	Gastroenterology 123:1485-1493(2002).
DR	EMBL, AF422457; AL24769.1; -.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0019028; C:viral capsid; IEA.
DR	GO; GO:0019031; C:viral envelope; IEA.
DR	GO; GO:0019198; F:structural molecule activity; IEA.
DR	InterPro: IPR002519; HCV env.
DR	InterPro: IPR002531; HCV NS1.
DR	Pfam: PF01539; HCV env; I.
KW	Coat protein; Envelope protein; glycoprotein; Nonstructural protein;
KW	Polypotein; Transmembrane.
FT	NON_TER 1
FT	CHAIN <1>154 envelope glycoprotein EI/E2.
FT	NON_TER 154
SQ	SEQUENCE 154 AA; 16737 MW; 9E5EB98BD5C189F CRC64;
Query Match	99.5%; Score 184; DB 2; Length 154;
Best Local Similarity	97.1%; Pred.No.1.9e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 STPGHITGHMAMDMNMMSPTTALVVSQILRI 34
Db	22 STPGHITGHRMAMDMMNSPTTLVVSQLRV 55
RESULT 36	
O91605	PRELIMINARY; PRT; 154 AA.
ID	O91605
AC	O91605:
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Polypotein (fragment).
OS	Hepatitis C virus.
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC	Hepadnavirus.
OX	NCBI_TaxID=11103;
OX	[1]
RN	SEQUENCE FROM N.A.
RX	MEDLINE=2229160; PubMed=12404223;
RA	Lya A.C., Fan X., Lang D.M., Yustin K., Ramrakhtiani S., Brunt E.M.,
RA	Korber B., Perelson A.S., Di Bisceglie A.M.;
RT	"Evolution of hepatitis C viral quasispecies after liver
RT	transplantation";
RL	Gastroenterology 123:1485-1493(2002).
DR	EMBL, AF422394; AL24706.1; -.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0019028; C:viral capsid; IEA.
DR	GO; GO:0019031; C:viral envelope; IEA.
DR	GO; GO:0019198; F:structural molecule activity; IEA.
DR	InterPro: IPR002519; HCV env.
DR	Pfam: PF01539; HCV NS1; I.
KW	Coat protein; Envelope protein; glycoprotein; Nonstructural protein;
KW	Polypotein; Transmembrane.
FT	NON_TER 1
FT	CHAIN <1>154 envelope glycoprotein EI/E2.
FT	NON_TER 154
SQ	SEQUENCE 154 AA; 16737 MW; 9E5EB98BD5C189F CRC64;
Query Match	99.5%; Score 184; DB 2; Length 154;
Best Local Similarity	97.1%; Pred.No.1.9e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	

Qy	1	SIYGHITGHRMADMMNNMSPTALVVSQRLRI	34
Db	22	SIYGHITGHRMADMMNNMSPTALVVSQRLRI	55

RESULT 37			
Q91609	PRELIMINARY;	PRT;	154 AA.
ID	Q91609		
AC	Q91609;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	Polyprotein (Fragment).		
OS	Hepatitis C virus.		
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepaciviruses.		
OX	NCBI_TaxID=11103;		
XX	[1]		
XP	SEQUENCE FROM N.A. PubMed=12404223;		
FX	MEDLINE=22291660; Lang D.M., Yusim K., Ramrakhiani S., Brunt E.M., Lyra A.C., Fan X.,		
RA	Korber B., Perelson A.S., Di Bisceglie A.M.; "Evolution of hepatitis C viral quasispecies after liver transplantation.";		
RT	Gastroenterology 123:1485-1493 (2002).		
RL	EMBL; AF422380; AA124702.1		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0019028; C:viral capsid; IEA.		
DR	GO; GO:0019031; C:viral envelope; IEA.		
DR	GO; GO:0005198; F:structural molecule activity; IEA.		
DR	InterPro; IPR002519; HCV env.		
DR	InterPro; IPR002531; HCV_NSI.		
DR	Pfam; PF01519; HCV env; I.		
DR	Pfam; PF01560; HCV_NSI. 1.		
KW	Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.		
KM	NON TER 1		
FT	CHAIN <1 154		
FT	NON TER 154		
FT	NON TER 154		
SO	SEQUENCE 154 AA; 16723 MW; D1480498B26A459 CRC64;		

Qy	1	SIYGHITGHRMADMMNNMSPTALVVSQRLRI	34
Db <td>22<th>SIYGHITGHRMADMMNNMSPTALVVSQRLRI</th><th>55</th></td>	22 <th>SIYGHITGHRMADMMNNMSPTALVVSQRLRI</th> <th>55</th>	SIYGHITGHRMADMMNNMSPTALVVSQRLRI	55

RESULT 38			
Q916RO	PRELIMINARY;	PRT;	154 AA.
ID	Q916RO		
AC	Q916RO;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	Polyprotein (Fragment).		
OS	Hepatitis C virus.		
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepaciviruses.		
OX	NCBI_TaxID=11103;		
XX	[1]		
XP	SEQUENCE FROM N.A. PubMed=12404223;		
FX	MEDLINE=22291660; Lang D.M., Yusim K., Ramrakhiani S., Brunt E.M., Lyra A.C., Fan X.,		
RA	Korber B., Perelson A.S., Di Bisceglie A.M.; "Evolution of hepatitis C viral quasispecies after liver transplantation.";		
RT	Gastroenterology 123:1485-1493 (2002).		
RL	EMBL; AF422389; AA124701.1		
DR	GO; GO:0016021; C:integral to membrane; IEA.		

DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env.
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01539; HCV_env; 1.
 DR Pfam; PF01560; HCV_NSI; 1.
 KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KM Polyprotein; Transmembrane.
 FT NON TER 1 1
 FT CHAIN <1 >154 envelope glycoprotein E1/E2.
 FT NON TER 154 154
 SQ SEQUENCE 154 AA; 16737 MW; 9E56B98BD5C189F CRC64;

Query Match 99.5%; Score 184; DB 2; Length 154;
 Best Local Similarity 97.1%; Pred. No. 1.9e-17;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
 DB 22 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 55

RESULT 39
 Q916R1 PRELIMINARY; PRT; 154 AA.

AC Q916R1; 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 CX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22291660; PubMed=12404223;
 RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramrakhiani S., Brunt E.M.,
 RA Korder B., Petersen A.S., Di Bisceglie A.M.;
 RT "Evolution of hepatitis C viral quasispecies after liver
 RT transplantation."
 RL Gastroenterology 123:1485-1493 (2002).
 DR EMBL; AF422388; AAL24700.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env.
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01539; HCV_env; 1.
 DR Pfam; PF01560; HCV_NSI; 1.
 KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KM Polyprotein; Transmembrane.
 FT NON TER 1 1
 FT CHAIN <1 >154 envelope glycoprotein E1/E2.
 FT NON TER 154 154
 SQ SEQUENCE 154 AA; 16737 MW; 9E56B98BD5C189F CRC64;

Query Match 99.5%; Score 184; DB 2; Length 154;
 Best Local Similarity 97.1%; Pred. No. 1.9e-17;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
 DB 22 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 55

RESULT 40
 Q916R2 PRELIMINARY; PRT; 154 AA.
 AC Q916R2;
 DT 01-DEC-2001 (TRENBLREL. 19, Created)

DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 CX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22291660; PubMed=12404223;
 RA Lyra A.C., Fan X., Lang D.M., Yusim K., Ramrakhiani S., Brunt E.M.,
 RA Korder B., Petersen A.S., Di Bisceglie A.M.;
 RT "Evolution of hepatitis C viral quasispecies after liver
 RT transplantation."
 RL Gastroenterology 123:1485-1493 (2002).
 DR EMBL; AF422387; AAL24699.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env.
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01539; HCV_env; 1.
 DR Pfam; PF01560; HCV_NSI; 1.
 KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KM Polyprotein; Transmembrane.
 FT NON TER 1 1
 FT CHAIN <1 >154 envelope glycoprotein E1/E2.
 FT NON TER 154 154
 SQ SEQUENCE 154 AA; 16771 MW; 70B2ASD8CDF61895 CRC64;

Query Match 99.5%; Score 184; DB 2; Length 154;
 Best Local Similarity 97.1%; Pred. No. 1.9e-17;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 34
 DB 22 SIYPGHITGHRMAMDMNMNSPTTALVVSQILRI 55

Search completed: November 10, 2004, 18:17:54
 Job time: 195 secs

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